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P23253;
01-NOV-1991 (Rel. 2
01-NOV-1991 (Rel. 2
20-AUG-2001 (Rel. 4
SIALIDASE (EC 3.2.1
TCNA.
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                   TRYCR
                                                                                                                                                                EMBL; M61732; AAA30255.1;
PIR; JH0557; JH0557.
HSSP; P29768; 1DIL.
                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The Trypanosoma cruzi neuraminidase contains bacterial neuraminidases, YWTD repeats of the receptor, and type III modules of fibronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-SILVIO X-10/4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              викатуота; Euglenozoa;
NCBI_TaxID=5693;
                                                                                                                               InterPro; IPR002860; BNF Pfam; PF02012; BNR; 2. Hydrolase; Glycosidase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pereira M.E.A., Mejia J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trypanosoma cruzi.
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MISCELLANEOUS: THE VARIABLE LENGTHS OF THE LONG TANDEM REPEAT DOMAIN COULD ACCOUNT IN PART FOR THE POLYMORPHISM OF THE TNCA
                                                                                                                                                                                                                                                                                                        SIMILARITY:
SIMILARITY:
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174:179-191(1991).
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                                                                                                                                                                                                                                                                                                        BELONGS TO FAMILY 33 OF GLYCOSYL HYDROLASES CONTAINS 3 BNR REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20, Created)
20, Last sequence update)
40, Last annotation update)
.1.18) (NEURAMINIDASE) (NA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=1896773;
a J.S., Aji T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=1711561;
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                                                                                                                               Glycoprotein;
CYS-RICH.
BNR 1.
BNR 2.
BNR 3.
FIBONECTIN TYPE-III.
44 X 12 AA TANDEM REPEATS, LTR DOMAIN.
N-LINKED (GLCNAC. . .) (POTENTIAL).
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neuraminidase
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                                                                                                                               Repeat;
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nidase on
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                                                                                                                                GPI-anchor;
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Best Local
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Q02910;
Q1-OCT-1993
Q1-OCT-1993
Q1-FEB-1994
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                                                                          SEQUENCE FROM N.A.
STRAIN-CANTON-S;
MEDLINE-9316572; PubMed-8094559;
MARTLINE-9316772; PubMed-8094559;
MARTLINING-931672; PubMed-8094559;
MARTLINING-931672;
MARTLINI
                                                                                                                                                                                                                                                        Pterygota; Neoptera; Endopterygota; Diptera; Ephydroidea; Drosophilidae; Drosophila. NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                        CPN OR CAP
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SEQUENCE FROM N.A. STRAIN=CANTON-S;
                                                                                                                                                                                                                                                                                                                                        Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                      CALPHOTIN
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27, Last sequence 28, Last annotations.
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                                                                                                                                                                                                                                                                                                                                      nropoda; Tracheata; Hexapoda; Insecta;
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No. 3.
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                                                                                                                                                                                                                                                                                                                Brachycera;
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Query Match
Best Local S
Matches 233
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Calclum-binding.
CONFLICT 36
CONFLICT 43
CONFLICT 64
CONFLICT 100
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CONFLICT 154
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CONFLICT 534
CONFLICT 703
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PIR; /
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c. Natl. Acad. Sci. U.S.A. 90:1536-1540(1993),
c. Natl. Acad. Sci. U.S.A. 90:1536-1540(1993),
c. NCTION: MIGHT FUNCTION AS A CALCIUM-SEQUESTERING "SPONGE" TO REGULATE THE AMOUNT OF FREE CYTOPLASMIC CALCIUM. IT BINDS 0.3 MOF CA+2 PER MOL OF PROTEIN.
SUBUNIT: HOMODIMER (PROBABLE),
SUBCELLULAR LOCATION: CYTOPLASMIC; HYPODENSE COMPARTMENT.
71SSUE SPECIFICITY: SOMA AND AXONS OF PHOTORECEPTOR CELLS OF COMPOUND EYES AND OCELLI.
DEVELOPMENTAL STAGE: EXPRESSED EARLY IN PHOTORECEPTOR CELL
DEVELOPMENT
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                                                             ETPALAPVVAESQVAANTVVATPPTPAPEPETIAPPVVAETPEVASVAVAETTPPVVPPV
                                                                                                                                         PLAAAEPVVVAPPATETPVVAPAAASPHVSVAPAVETAVVAPVSASTEPPVAAATLTTAP
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Pred. No. 3.1e-14;
3; Mismatches 433
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                                                                                                                                           DIAIPVIDPPVPQEIAVAEIPETDTKPAEVIVEQSTIPIEAPVPEVSKYAEPVISEAPAA
                                                                      EVPITAGDNPDNTSVGISEVVPTIAEKPVEEVPTS--EIPEQSSSPS--DSVPVAKITPL
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                                                                              its evolutionary implications.";

J. MOI. Evol. 43:348-356(1996).

-i. FUNCTION: PROVIDES ADHESIVENESS TO THE MUSSEL'S FOOT. MUSSEL'S PRODUCE ONE OF THE STRONGEST WATER INSOLUBLE GLUE. THE MUSSEL'S ADHESIVE IS A BUNDLE OF THREADS, CALLED A BYSSUS, FORMED BY A FIBROUS COLLAGEBOUS CORE COATED MITH ADHESIVE PROTEINS.

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30-MAY-2000
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This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics
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Harayama S.;
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                     IHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKT---
                                                                                                             EPAPTTPKEPAPTTPKGTAPTTLKEPAPTTP----KKPAPKELAPTTTKGPTSTTSDKPA
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76; Conservative
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ADHESIVE PLAQUE MATRIX PROTEIN.
NONREPETIVE LINKER.
TANDEM REPEATS OF Y-K-[PS]-K-[IP]-{ST}-Y-P-[PST]-{ST}.
NONAPERTIDE 1.
NONAPERTIDE 2.
NONAPERTIDE 2.
MW; 98CC70D7C75FF3C4 CRC64;
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Pred. No. 8.5e-14;
PKISYPPTYK--
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RESULT
NFH_RAT
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                                                                                     Proc. Natl. Acad. Sci. U.S.A. 86:2463-2467(1989).

-!- FUNCTION: NEUROPILAMENTS USUALLY CONTAIN THREE IF PRO AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURON NF-H HAS AN IMPORTANT FUNCTION IN MATURE AXONS THAT I SUBSERVED BY THE TWO SMALLER NF PROTEINS.

-!- PTM: THERE ARE A NUMBER OF REPEARS OF THE TRIPEPTIDE PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOT THOUGHT THAT PHOSPHORYLATION OF NFH RESULTS IN THE FO INTERFILMMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE
                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 318-831 FROM N.A.

MEDLINE-89184647; PubMed-2928342;

Lieberburg I., Spinner N., Snyder S., Anderson J., Goldgat

Smulowitz M., Carroll Z., Emanuel B.S., Breitner J., Rubin

"Cloning of a CDWA encoding the rat high molecular weight
neurofilament peptide (NF-H); developmental and tissue ex-

che rat, and mapping of its human homologue to chromosomes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Robinson P.A., Wion D., Anderton I "Isolation of a CDNA for the (NF-H)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1990 (Rel. 15, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT).
(NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H) (FRAGMENT).
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P16884;
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Breen K.C., Robinson P.A., Wion D., Anderton B.H
"Partial sequence of the rat heavy.neurofilament
Identification of putative phosphorylation sites
FEBS Lett. 241:213-218(1988).
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Mammalia; Eutheria; Rodentia;
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HE LARGER NEUROFILAMENT PO
LS OF PHOSPHORYLATION BEIN
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-Dinh D., Roussel
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Sciurognathi; Muridae
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SL; X13804; CAA32038.1; A

SL; W121964; AAA41695.1; -

SL; J04517; AAA41692.1; -

R1; A36796; A30796.

R2; A36796; A36796.

R3; B25649; A25649.

R3; B25649; B25649.

R3; S02003; S02003.
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"P-domains as shuffled cysteine-rich
C.1 (FIM-C.1) from Xenopus laevis. Po
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01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
101-OCT-1994 (Rel. 30, Last annotation update)
1NTEGUMENTARY MUCIN C.1 (FIM-C.1) (FRAGMENT).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                         TISSUE=Skin;
MEDLINE=93077556; PubMed=1447205;
                                     or send
                                                modified and this statement is not removed entities requires a license agreement (See
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01-OCT-1994
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                                                                                       European
                                                                                                                                           SIMILARITY: CONTAINS 6 P-TYPE (TREFOIL) DOMAINS
                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                           Bioinformatics Institute. The profit institutions as long
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EMBL; L02115; PIR; A45155;

AAA74725.1;

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Query Match
Best Local Sim
Matches 223;
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InterPro; IPR000519; P_trefoil.
Pfam; PF00088; trefoil; 6.
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  Similarity 28.1
23; Conservative
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P-TYPE 4.
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P-TYPE 5.
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BY SIMILARITY.
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P-TYPE 3.
12 X APPROXIMATE 7
THR-RICH.
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 Score 509.5; DB 1;
Pred. No. 1.5e-13;
18; Mismatches 276;
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p-TYPE
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DNA-DIRECTED
POLR2A.
                           Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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P24928;
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                 NCBI_TaxID=9606;
SEQUENCE
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l. 21, Last sequ
l. 40, Last anno
A POLYMERASE II
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Primates;
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annotation update)
E II LARGEST SUBUNIT
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                             Craniata; Vertebrata; Catarrhini; Hominidae;
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Best Local S
Matches 181
  1625
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Transferase; DNA-directed RNA polymerase; Transcription; Zinc; DNA-Dinding; Nuclear protein; Phosphorylation; Zinc-finger.

ZN_FING 71 87 C2H2-TYPE (POTENTIAL).

ZN_FING 1958 CARBOXYL-TERMINAL 7-RESIDUE REPEAT CONFLICT 1067 1067 W -> L (IN REF. 2).

CONFLICT 1449 1449 D -> Y (IN REF. 2).
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[2]
                                                                                                                                                                                                                                       SEQUENCE
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Mita K., Tsuji H., Morimyo M., Takahashi E., Ne
Ichimura S., Yamauchi M., Hongo E., Hayashi A.;
"The human gene encoding the largest action."
                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S21054; S21054.
MIM; 180660; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long a modified and this statement is not removed.
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InterPro; IPR000722; RNA_pol_A.
InterPro; IPR002879; RNA_pol_A2.
                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a
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                            424
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SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                             X63564; CAA45125.1;

X74874; CAA52862.1;

X74873; CAA52862.1;

X74872; CAA52862.1;

X74871; CAA52862.1;

X74870; CAA52862.1;

X74870; CAA52862.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THE PHOSPHORYLATION ACTIVATES POL2.
MISCELLANEOUS: THREE DISTINCT ZINC-CONTAINING
FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR 1
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TSPSY-SPTSPNYSPTSPSY-SPTSPSY-SPTSPSY---
                                                     PTPGSPGSPGPSSPYIPSPGGAMSPSYSPTSPA-YEPRSPGGYTPQSPSYSPTSPSY-SP
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                                                                                                                                                                               Similarity
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Acids Res.
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(See http://www.isb-sib.ch/announce/

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Mammalia; Eutheria; Primates; Catarrhini;
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                                                                                                                 LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION.

SIMILARITY: BELONGS TO THE INTERNEDIAN ETT.
                                                                                                                                                                    PTM: PH
OF THE
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PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P, PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF. IT
                                                                                                                                                                                               THOUGHT THAT PHOSPHORYLATION OF NFH RESULTS IN INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT OF AXONAL CALIBER.
                                                                                                                                                                                                                                                                                                               structure and organization of the human heavy nit (NF-H) and the gene encoding it.";
J. 7:1947-1955(1988).
                                                                             SWISS-PROT entry is copyright. It is produ
een the Swiss Institute of Bioinformatics
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MENT HEAVY POLYPEPTIDE) (NF-H).
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Search completed: April 26, 2002, 16:32:55 Job time: 605 sec

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NESULT 1 US-09-103-429A-4 ISEQUENCE 4. APPLICANT: Granados, Robert R APPLICANT: A No. 6187558th Tioga CITY: Thaca CITY: Thaca CITY: Thaca COMPTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPTER READABLE FORM: COMPTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPTER READABLE FORM: COMPTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPTER READABLE FORM: MEDIUM TYPE: GRANATION: COMPTER READABLE FORM: MEDIUM TYPE: GRANATION: APPLICANTION UNMERE: 10,709/103,429A FILECOMUNICATION DATA: APPLICANTION UNMERE: 14,390 CORRENT APPLICATION UNMERE: 13,390 TELECHONE: (607) 256-3200 TELEPAN: (607) 256-3200 TELE	28 404.5 5.5 408 4 US-08-475-411A-65 Sequence 65, Appl 398.5 5.5 682 1 US-08-6478-029A-65 Sequence 25, Appl 398.5 5.5 682 1 US-08-642-255-126 Sequence 36, Appl 398.5 5.5 682 1 US-08-325-267A-2 Sequence 37, Appl 387 5.3 1231 3 US-08-304-235A-36 Sequence 27, Appl 381 5.2 1848 4 US-08-296-791-6 Sequence 4, Appl 398.5 5.3 1284 5 PCT-US95-10661A-6 Sequence 6, Appl 398.5 5.1 1761 2 US-08-797-237A-84 Sequence 6, Appl 398.5 5.1 1761 2 US-08-707-237A-84 Sequence 84, Appl 398.5 5.1 1761 2 US-08-707-237A-84 Sequence 84, Appl 399.5 5.1 1762 1 US-08-842-255-114 Sequence 84, Appl 370.5 5.1 1187 1 US-08-642-255-62 Sequence 65, Appl 370.5 5.1 1187 1 US-08-320-559-28 Sequence 28, Appl 370.5 5.1 1187 5 PCT-US94-04496-28 Sequence 28, Appl 370.5 5.1 1187 5 PCT-US94-04496-28 Sequence 28, Appl 370.5 5.1 1210 1 US-08-320-559-26 Sequence 26, Appl 370.5 5.1 1210 1 US-08-320-559-26 Sequence 26, Appl 370.5 5.1 1210 1 US-08-320-559-26 Sequence 26, Appl 370.5 5.1 1210 1 US-08-320-559-26 Sequence 28, Appl 370.5 5.1 1210 1 US-08-320-559-26 Sequence 26, Appl 370.5 5.1 1210 1 US-08-320-559-26 Sequence 26, Appl 370.5 5.1 1210
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Query Match Best Local Similarity

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RESULT 2
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APPLICANT: Peters
                                      TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS, TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM NUMBER OF SEQUENCES: 30

CORRESCONDENCE: 30
                                  CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                          TTAVPEIPTT-----VTSPPTAAPTT-AAPAPNT-----
                                                                                                                                                                                                                                                                                                                                                       AP----NTTVTAPPTAAPTT-AAPAPNTTVTVPPTAAPTAAP-----PTVAH-----
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E: PETERS, VERNY, JONES & BIKSA
385 Sherman Avenue, Suite 6
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; MOLECULE TYPE: protein
US-08-928-361B-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 60/026
FILING DATE: 13-SEP-1996
AFFORNEY/AGENT INFORMATION:
NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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LENGTH: 1837 amino aci
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                    TQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPT 331
                                                                                                                                                                                                                                                                                                                                                                                                      PNSDTSKETSLTVNKET-----TVETKETTTTNKQTST-----DGK-----EKTTSAKE 271
                                                                                                                                                                                                                                                                                                                                                                                                                                               GWKQ-----TGLPTDPYPNCP
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                    KKPTTTTTATTTTTSETESVIKPDEWCWLEKNGECEAKGATYVGVIGKDGRIENGMAFT
                                                       KEPSPTTTKEPAPTTPKEPAPTTPKK-----
                                                                                                                         PAPTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTP 511
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                                                                                        US/08/928,361B
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RESULT 3
5202236-25
; Patent No. 5202236
; Patent No. 5202236
; APPLICANT: MAUGH, KATHY J.; ANDERSON, DAVID M.; STRAUSBERG, SUSAN L.; MCCANDLISS, RUSS, WEI, TENA; FILPULA, DAVID
; TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
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NUMBER OF SEQUENCES: 39
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-MAY-1990
APPLICATION NUMBER: 82,456
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APPLICATION NUMBER: 933,945
FILING DATE: 24-NOV-1986
APPLICATION NUMBER: 650,128
APPLICATION NUMBER: 650,128
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LENGTH: 744
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RESULT 4 US-08-700-651-5

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CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT FILING DATE: 1997-08-14
EARLIER FILING DATE: 1997-08-14
EARLIER FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: NELSON, RICHARD,
APPLICANT: GUT, JIRI
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                                                                                                                                        GTTKPKPGIPVNGGGVVPDEEAKDQADKGKDGLIVPPTNSINKDPVTNTQYSNTTGNI--
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                                                                                                                                                                                                                                                                                                                    TTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKP--EETAKPKD------RATNSKATT
                                   -MLSDETNICNGK--
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RESULT 5
US-09-103-429A-3
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                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                ZIP: 14850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                 APPLICANT: Wang, Ping
TITLE OF INVENTION: A No. 6187558el I
TITLE OF INVENTION: CDNA and Related
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                     STATE:
APPLICATION NUMBER: US/0 FILING DATE: 24-JUN-1998
                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                    14850
                                                                                                                                                                                   Ithaca
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                                                                                                                                                                                                   E: Brown, Pinnisi & Michaels, P.C. 118 No. 6187558th Tioga
                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                     Granados,
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                 US/09/103,429A
                                                    Version
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US-09-103-429A-3

MOLECULE TYPE: HYPOTHETICAL: N ANTI-SENSE: NO

TELEBAX: (607) 256-3628
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 786 amino acids

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TYPE: amino acid

STRANDEDNESS: TOPOLOGY:

linear : protein single TELECOMMUNICATION INFORMATION: TELEPHONE: (607) 256-2000

ATTORNEY/AGENT INFORMATION:

CLASSIFICATION:

NAME: Michaels, Christopher A REGISTRATION NUMBER: 34,390 REFERENCE/DOCKET NUMBER: BTI-

DЬ

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Query Match

6.8%; Score 498.5; DB 4;
Best Local Similarity 29.1%; Pred. No. 1.8e-24;
Matches 200; Conservative 25; Mismatches 207;
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ORGANISM: Trichoplusia ni
TISSUE TYPE: peritrophic membrane
                                778 DKPAPTTPKETAPTTPKEPAPTTPKKP 804
                                                                     633 TAAPTT-AAPAPUTTVTVPPTAAPTAAPPTVAH------APUTTAAPVTTTS
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                                                                                                            GTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTS 777
                                                                                                                                                                                                                                    --PAPTAAPTAAPTTAAPESPTTVTVP-PTAAPTAAPTTAVPEIPITVT---SAPTAAPT
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                                                                                                                                                                                                                                                                                                                   NQCTSTAAPTAAPTAAPTAAPTA---APSTVVPPATPPATAAPVPPTT---AIPT--
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                                                                                                                                                      AAPTAAPTAAPTTAVPEIPTTVTSPPTAAPTTAAP---APNTT-------VTVPP 632
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US-08-928-361B-6
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Best Local Similarity
Matches 300; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
TOPOLOGY: lir
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 650-324-1678 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Petersen, OF TITLE OF INVENTION: PRITITLE OF INVENTION: PRITITLE OF INVENTION: SINUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY_AGENT INFORMATION:
NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 650-324-1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
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ADDRESSEE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
                                302 KGPALITPKEPTPTTPKEPASTTPKEPTPTTIKSAPTTPKEPAPTTTKSAPTTPKEPAPT 361
      212
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REFERENCE/DOCKET NUMBER: 48
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                                                                                                                                                        YAGVYRSNETKTTEPSANTNFLLVDPKINAPCNSENSFEQGQIFDMGSKVYIPYTKCVGV 189
                                                                                                                                                                                               HNKVSTSPKITTAKP-----INPRPSLPPNSDTSKE-----TSLTVN 241
                                                                                                                                                                                                                                                                                --SKNSAANRELQKKLKVKDNKKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQ 204
KETTVETKETTTINKQTSTDCKEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTT 301
                                                                                                                                                                                                                                        DPYSNCPFN-----PVTGNLVSRSTGKTIPN----TYAGVYRSN-ETKTTEPSANT-- 129
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PEPTIDES,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08928361B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTTVPTT----TTTTKRDEMTTTTPLPDIGDIEITPIPIEKMLDKYTRMIYDYNSGL
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                                                                                                                                                                                PSTGKPINNSTAGIVSGKPGLPPIEDENGNLEDPSTNLPIDGNNQLVNPETNSTVSGSTS
                                                                                                                                                                                                                                            INPTNNNTMDSSFAGAYKYAVSNGIKTDNVYGLPVGEITGLPKDPGSDIPFNSTTGELVD 1054
                                                                                                                                                                                                                                                                         TTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKP--EETAKPKD------RATNSKATT
                                                                                                                                                                                                                                                                                                        LMYDIESGRLIGQVSKRPIPGSIAGDLNPIMKTPTQTDSVTGKPIDPTTGLPFNPPTGHL
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                                                                                    VEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPD-----MDYLPRVPNQGIIINP--
                                                                                                                      {\tt GTTKPKPGIPVNGGGVVPDEEAKDQADKGKDGLIVPPTNSINKDPVTNTQYSNTTGNI---}
                                                                                                                                                    --TMPE----
                                                                                                                                                                                                              PKPQKPTKAPKKPTSTKKPKTMP-----
                                                           -ETGKVIPGSLPGSLNYPSFNTPQQTDEITGKPVDTVTGLPYDPSTGEIIDPAT
                                                                                                                                                                                                                                                                                                                                                                                                ---PELSAEPTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTER---
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                            -MLSDETNICNGK--------PVDGLTTLRNGTLV 1125
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 153; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (301) 295-4033
INFORMATION FOR SEQ ID NO: ...
SEQUENCE CHARACTERISTICS:
LENGTH: 826 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
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TITLE OF INVENTION: im
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Spevack, Avrom D. TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 295-6759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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SNPNE - - PLNPNEP - - - -
                   TTPEEPTPTTPEEPAPTTPKAAAPNTPKEP-APTTPKEPAPTTPKEPAPTTPKETAPTTP 671
                                                                                     PAPTITKKPAPTAPKEP-APTIPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAP 612
                                                                                                                                        RRNPKRRNPNKPKPNKPNPNKPNPNEPSNPNKPNPN-----EPSNPNKPNP-----NEPSN
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nilarity 26.4%;
Conservative 54
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Hedstrom, Richard
Khusmith, Srisin
Rogers IV, William O.
RVENTION: Protective malaria
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                                                                                                                                                                                                                                                                                                                                                                       Score 488.5; DB 1;
Pred. No. 8.5e-24;
4; Mismatches 223;
                                                                                                                           -EPLNPNEPSNPNEPSNPNAPSNPNE--PSNPNE 492
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NAME: Spevack, Avram D.

TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 295-6759
TELEFAX: (301) 295-4033
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 826 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US92-00018-2
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PCT-US92-00018-2
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                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 6.7%; Score 488.5; DB 5; Best Local Similarity 26.4%; Pred. No. 8.5e-24; Matches 153; Conservative 54; Mismatches 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Applicati
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSE: A. David Spevack
STREET: NMRDC Building 1 T-12 National Naval
STREET: Medical Center
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APPLICANT: Hedstrom, Richard
APPLICANT: Khusmith, Srisin
APPLICANT: Rogers IV, William O.
                 438
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                                                                                             333
                                                                                                                                                     382 PAPTTTKSAPTTPKEP-APTTPKKP-APTTPKEP-APTTPKEP-TPTTPKEPAPTTKEPA 437
                                                                                                                                                                                                                                     273 TPCKVRDCPQIPIPPVIPNKIPEKPSNPEEPVNPNDPNDPNNPNNPNNPNNPNNPNNPNN 332
                                                                                                                                                                                                                                                                                                                      329 TPTTIKSAPTTPKEPA-PTTTKSAPTTPKEPA-PTTTKEP----APTTPKEP-APTTTKE 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       650 LPIIPQKGNNIPSNLPENPSDSEVEYPRPNDNGENSNNTMKSKKNI---PNEPIPSPGDN 706
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ZIP: 20814-5044
PTTPKEPAPTAPK--KPAPTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTT 495
                                                                            PKEPI------NPEESNPKEP----INPEDNENPLIIQDEPIEPRNDSNVIPI 649
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                                                                                                                                                                                                                                                                                                                                                                                                           Indels 149;
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	TTTKSAPTTPKEPAPTTPKKPAPT-TPKEPAPTTPKEPTPTTPKEPAPTTKEPAPT 439	139 PT	dd Vy	
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	TQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKE 327	272 T	Qy	
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	TTAKPINPRPSLPPNSDTSKETSLTVNKET	212 F	Qy	
4s Un	6.5%; Score 476.5; DB 6; Length 652; Similarity 29.7%; Pred. No. 3.8e-23; Conservative 71; Mismatches 284; Indels 169; Gaps	Query Match Best Local & Matches 221	X # O	
	тн: 652	LENGTH:)2236-13	; 5202	
	NG DATE: 13-SEP-1984	FILI FILI	ດ	
	NG DATE: 24-NOV-1986 ICATION NUMBER: 650.128	APPI		
	NG DATE: 07-AUG-1987 ICATION NUMBER: 933 945	APPI APPI		
	DATE: 25-MAY-1990	FILING		
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	ETHOD	TITLE	; ; PF	
	;ANDERSON, DAV	12236-13 ntent No. APPLIC	520 ; Pa ; Su	
		SULT 9	RES	
	YKGHEERIPKPHRSNDDYVYDNNVNKNNKDEPEIPNNE 745	707 P	Ф	
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	TTDEEPTPTTPEEPAPTTPKAAAPNTPKEP-APTTPKEPAPTTPKEPAPTTPKETAPTTP 671	613 7	Оу	
		493 1	Db	
	PTTTKKPAPTAPKEP-APTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTT	554	Qy	
	PNKDNPNEPSNPNKPNPNEPLNPNEPSNPNEPSNPNAPSNPNEPSNPNE 492	444	Дb	
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                                                                                                                                                           SOFTWARE: Pat
SEQ ID NO 5
LENGTH: 960
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/09219849 Patent No. 6150081
Best Loc
Matches
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APPLICANT:
                             Query Match
                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/219,849
CURRENT FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 50
                                                                                                                                                                                                                                                                       APPLICANT: VAN DEN BOSCH, TANJA J.
TITLE OF INVENTION: SILVER HALIDE EMULSIONS WITH RECOMBINANT COLLAGEN
TITLE OF INVENTION: SUITABLE FOR PHOTOGRAPHIC APPLICATION AND ALSO TH
TITLE OF INVENTION: PREPARATION THEREOF
FILE REFERENCE: 2728-2
                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                            FEATURE:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                            ORGANISM: Artificial Sequence
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Local Similarity
nes 173; Conserv
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VAN RIIN, ALEXIS C.
BOUWSTRA, JAN B.
DE WOLF, FREDERIK A.
MOOBROEK, ANDREAS
WERTEN, MARC W.T.
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                                                                                                                                                                                                                                                                                                                                                    WIND,
Conservative
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                                                                                            Description of Artificial Sequence: Illustrative amino acid sequence
                6.2%;
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   60;
   Score 452; DB 4;
Pred. No. 2.2e-21;
60; Mismatches 309
    309;
                               Length
    Indels
                                    960;
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                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                           Sequence 23, Application Patent No. 6235872 GENERAL INFORMATION:
CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                          COMPUTER READABLE FORM
                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                          MEDIUM TYPE: Floppy disk
                                                                                                          ZIP:
                                                                                                                        COUNTRY:
                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                       SRDPGPPGAHGPAGPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPKEPA-----PTTPKET-APTTPKGT-----APTTLKEPAPTTPKKP-APKELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SRDPGPPGAPGPAGPPGSRDPGP--PGAPGPPGSRDPGPPGAPGPPGSRDPGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPPGSRDPGP-----PGAPGPAGPPGSRDPGP--PGAPGPAGPPGSRDPGP--PGAPGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGPAGPPGSRDPG--PPGAPGPAGP--PGSRDPGPPGAPG-PAGPPGSRDPGPPGAPGPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEKPAPT-TPEELAPTTPEEPTPTTPEEPAPTTPKAAA-PNTPKEPAPTTP---KEPAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGPPGSRDPGPPGAPGPAGPPGSRDPGPPGAPGPAGPPGSRDPGP----PGAPGPAGPPG
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                                                                                                           92122
                                                                                                                                                       San Diego
                                                                                                                       California
: United States
                                                                                                                                                                     E: Campbell & 4370 La Jolla
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                                                                                                                                                                                                                                                                              Bredesen,
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a Village Dri
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and Methods of
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NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 9-LJ 26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 1185 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-041-886-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
         619
                                715 TPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTS 774
                                                                                                                                             501 NSGPPPPGAFPHPLEGGSSHHAHPYAMSPSLGSLRPYPPGPAHLPPPHSQVSYSQAGPNG
                                                                                                                                                                                                                     441 GPPPPPPYGRLLANSNAHPGPFPPSTGAQSTAHPPVSTHHHHHQQQQQQQQQQQQQQQHHG
                                                                                                                                                                                                                                                       588 --PTTPE--KLAPTTPEKPAPTTPEELAPTTPEEPTPT--------------
                                                                                                                                                                                                                                                                                                    392
                                                                                                                                                                                                                                                                                                                               532 PTTPKKPAPTTPKEPAPTTPKE-PAPTTTKKPAPTAPKEPAPTTPKETAPTTPKKLT---
                                                                                                                                                                                                                                                                                                                                                                    335 MGQGMGGLPPGP---EKGPTLAPSPHSLPPASSSAPAPPMRFPYSSSSSSAAASSSSSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 VSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETTVETKETTTTNKOTSTDGKEKTT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88 SQTIKSTTKRSPKPPNKKKTKKVIESEEITEEHSVSENQESSSSSSSSSSSSTIWKIKSS 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 SMSMRSGRKKEAPGPR------EELRSRGRASPGGVSTSSSDG-----KAEKS
SPAGYKTASPPGPPPYGKRAPSPGAYKTATPPGYKPGSP-----PSFRTGTPPGYRG--- 670
                                                                                                      PAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAP---TTTKEPTSTTSDKPAPT
                                                                     PPVSSSSNSSSSTSQGSYPCS--HPSPSQGPQGAPYPFPPVPTVTTSSATLSTVIATVAS
                                                                                                                                                                                                                                                                                            SSSSASPFPAS--QALPSYPHSFPPPTSL----SVSNQP----PKYTQPSLPSQAVWSQ 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIYSPGSVENDS------DSSSGLSQGPA--RPYHPPPLFPPSPQPPDSTP 176
                                                                                                                                                                                  --TPEEPAP-----APTTPKAAAPN----TPKEPAPTTPKEP-----APTTPKE 657
                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGNLPSAPPPANFPHVTPNLPPPPALRPLNNASASP----PGLGAQPLPGHL--PSPYA 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPAPTTKEPAP-----TTPKEPAPTA--PKKPAPTTPKEPAPTTTKEPSPTT 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGVLSGPPMGPKGGGAASSVGGPNGGKQHPPPTTPISVSSSGASGAPPTKP----PTTPV 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --TTKSAPTTPK-------EPAPTTPKKPAPTTPKEPAPTTPKEPTPTTPK 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ROPEASF-----EPHPSVTPTGYHAPMEP-PTSRMFQAP--PGAPPPHPQLYPGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEPTPTTIKSAPTTPKEPAPTTTKSAPITPKEPAPTTTKEPAPTTTKEPAPTTTKEPAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ETNAPKKTKTEQELPRPQSPSDLDSLDGRSL--NDDGSSDPRDIDQDNRSTS------P 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTP--KEPASTTP 325
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Best Local Similarity 23.7
Matches 255; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236 TSLTVNKETTVETKETTTINKQTSTDGKEKTTSAKETQSIEKTSAKD-LAPTSKVLAKPT 294
                                                                                                                                                                                 241
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 574 TPKETAP----TTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPT 629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
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LOCATION: 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                P-KAETTTKGP--ALTTPKEP-----TPTTPKEPASTTPKEPTPTTIKSAP 337
                                                                                                                                                                               APDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS
                                                                                                                                                                                                                                                      APDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS
                                                                                                                                                                                                                                                                                                                           ---DNKPAPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS 180
                                                                                                                                                                                                                                                                                                                                                                                              PGSGSSTTQGQDVTLAPATEPASGSAATWGQDVTSVPVTRPALGSTTPPAHDVT---SAP 122
                                     SAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVT
                                                                      PAPTTPKEPAPTTPK----KPAPTTPKEPAPTTPK----EPAPTTTKKPAPTAPKEPAPT
                                                                                                                                            TKEPSPTTPKEPAPTT--TKSAPTTTKEPAPTT----TKSAPTTPKEPSPTTTK----E
                                                                                                                                                                                                                   PKE--PAPTTKEP-----APTTPKEPAPTAPK----KPAPTTPKEPAPTTPKEPAPTT 472
                                                                                                                                                                                                                                                                                        TKE--PAPTTT-----KSAPTTPKEPAPTTPK----KPAPTTPKEPAPTTPKEPTPTT 425
                                                                                                          {\tt APDXRP-XPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVT}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1867 amino acids
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147
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1..21
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23.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "The amino acids spanning 128 to 1727 constitute a repeated region wherein the repeat 20 amino acids, 17 of which are fixed. The number of such repeats varies from 1 to 40."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Amino acid 134 is X1 = Xaa
which is the codon for Pro or Ala wherein Pro =
or CCG; and Ala = GCT, GCC, GCA, or GCG."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Amino acids 1 to 21 are a 21 amino acid precursor sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Amino acid 147 is X2 = Xaa which is the codon for Pro or Ala wherein Pro = or CCG; and Ala = GCT, GCC, GCA, or GCG."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Amino acid 144 is Y = Xaa which is the codon for Thr or Asn wherein or ACG; and Asn = AAT or AAC."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3%; Score 424.5; DB 2;
7%; Pred. No. 2.9e-19;
69; Mismatches 511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 241;
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RENT APPLICATION DATA: PPLICATION NUMBER: US/09/083,116 ILING DATE: LASSIFICATION:	
MEDIUM TYPE: Floppy disk MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTMADRE: DetentIn Release #1.0	
STATE: Virginia COUNTRY: United ZIP: 22313-1404	
A1	
TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES:	
APPLICANT: LATHE, Richard APPLICANT: HARBUYENI, Mara	~. ·. ·
GENERAL INFOR APPLICANT:	
LT 13 9-083-1 quence quence	· ` ;
Db 958 VTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPD 1003	₽
SPID 115	Ø
Db 912 APXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHG 957	Dk
QY 1045 -PNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLSD 1103	9
Db 869 -GSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSA-PDXRPXPGST 911	맜
QY 985 KPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPNQT 1044	8
Db 821 APDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXP- 868	맜
OY 925 TTTODTTPFKITTLKTTTLAPKYTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQ 984	20
: : : :	문
Qy 869 -TKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTS 924	Ó
703 DXRPXPGSTAPXAHGVTSAPDXRPXPGSTAP	д ;
823 TTTKEPTTI	Q Q
: 645 RPXPGS	Db
Oy 779 KPAPTIPKETAPTTPKEPAPTTPKKPAPTTPETPPPTTSEVSTP 822	δō
Db 586 PXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAP-XAHGVTSAPDX 644	Дb
APTTPKG	δŎ
Db 531 TAPXAHGVTSAPDXRPXPGSTAP-XAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXR 585	DЬ
Qy 685 TTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTP 732	VΩ
 472 APXAHGVT	밁
630 T	VQ
Db 420 SAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGST 471	DЪ

APPLICATION DATA:

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                                                                                                                                                                                                                                                             Query Match 5.8
Best Local Similarity 23.7
Matches 255; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1867 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: peptide
FEATHIRE: TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Peptide LOCATION: 147
OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,320
FILING DATE: 04-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/403,576
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
                123 --DNKPAPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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LOCATION: 128.1727
OTHER INFORMATION: //
OTHER INFORMATION: 11
OTHER INFORMATION: 21
OTHER INFORMATION: 21
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REGISTRATION NUMBER: 35,030
REFERENCE, DOCKET NUMBER: 017753-025
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-6620
                                                      338 TTPKEPAPTTT-----KSAPTTPKEP-----APTTTKEPAPTTPKEPAPTT 378
                                                                                                                                                                                                  236 TSLTVNKETTVETKETTTNKQTSTDGKEKTTSAKETQSIEKTSAKD-LAPTSKVLAKPT 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Peptide LOCATION: 134
OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                     295
                                                                                                                                                                             16 TVLTV-----VTGSGHASSTPGGEKETSATQRSSVPSSTEKNAVSMTSSVLSSHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION UNIMBER: WO PCT/FR91/00835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
                                                                                                                        P-KAETTTKGP--ALTTPKEP------TPTTPKEPASTTPKEPTPTTIKSAP 337
                                                                                              PGSGSSTTQGQDVTLAPATEPASGSAATWGQDVTSVPVTRPALGSTTPPAHDVT---SAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
144
                                                                                                                                                                                                                                                                                      5.8%;
                                                                                                                                                                                                                                                                                                                                                                               /note= "Amino acids 1 to 21 amino acid precursor s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Amino acid 147 is x2 = xaa
which is the codon for Pro or Ala wherein Pro = CCT, CCC,
or CCG; and Ala = GCT, GCC, GCA, or GCG."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Amino acid 144 is Y=Xaa which is the codon for Thr or Asn wherein Thr = ACT, ACC, or ACG; and Asn = AAT or AAC."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Amino acid 134 is X1 = Xaa
which is the codon for Pro or Ala wherein Pro = CCT, CCC, CC,
or CCG; and Ala = GCT, GCC, GCA, or GCG."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "The amino acids spanning 128 to 1727 constitute a repeated region wherein the repeat 20 amino acids, 17 of which are fixed. The number of such repeats varies from 1 to 40."
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                                                                                                                                                                                                                                                                 69;
                                                                                                                                                                                                                                                           Score 424.5; DB 4;
Pred. No. 2.9e-19;
9; Mismatches 511;
                                                                                                                                                                                                                                                                                                                                                                                 o 21 are a
sequence."
                                                                                                                                                                                                                                                                                                   Length 1867;
                                                                                                                                                                                                                                                           Indels 241;
                                                                                                                                                                                                                                                         Gaps
                                                                                              122
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Sequence 2, Application US/08479537A
Patent No. 5861381
GENERAL INFORMATION:
APPLICANT: CHAMBON, Pierre
APPLICANT: KIENY, Marie-Paule
APPLICANT: LATHE, Richard
APPLICANT: HAREUVENI, Mara
TITLE OF INVENTION: PHARMACEUTICAL
TITLE OF INVENTION: TREATMENT OR P
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70,6		_	2
	912 APXAHGVTSAPDXRPXPGSTAPXAH	Db 9	н
1103	45 -PNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLSD	Qy 1045	_
	869 -GSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSA-PDXRPX	Db 8	H
	985 KPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPNQT	Ωу 9	_
	821 APDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXP-	Db 8	_
984	925 TTTQDTTPEKITTLKTTTLAPKYTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQ	Qy 9	_
	763 DXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS	Db 7	_
	869 -TKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTS	Оу в	_
	703 DXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAP	Db 7	
868	823 TTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAA	Qy E	_
	645 RPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAP	Db (
P 822	779 KPAPTTPKETAPTTPKEPAPTTPKKPAPTTPETPPPTTSEVSTP	Qy :	
	586 PXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAP-XAHGVTSAPDX	Db .	
	733 KEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSD	Оy	
	531 TAPXAHGVTSAPDXRPXPGSTAP-XAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXR	Ъ	
	685 TTPKKPAPKELAPTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTP	Qγ	
	472 APXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRP-XPGSTAPXAHGVTSAPDXRPXPXGS	Db	
	630 TPKAAAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGT-APTTLKEPAP	Qy	
	420 SAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGST	В	
	574 TPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPT	Qy	
	360 SAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVT	Дb	
	522 PAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTTTKKPAPTAPKEPAPT	Qy	
	S.	Db	
E 521	473 TKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPKEPSPTTTK	Qy	
	241 APDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS	Ъ	
T 472	426 PKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAPTTPKEPAPTT	Qy	
	181 APDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS	DЪ	
T 425	379 TKEPAPTTTKSAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPTPTT	δÃ	

PHARMACEUTICAL COMPOSITION TREATMENT OR PREVENTION OF

FOR THE A MALIGNANT TUMOR

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MEDIUM TYPE: FLOPPY CLEAR
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,537A
FILING DATE: 07-UN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: FR 90/13101
FILING DATE: 23-OCT-1990
PRIOR APPLICATION NUMBER: WO PCT/FR91/00835
FILING DATE: 23-OCT-1991
PRIOR APPLICATION NUMBER: WO PCT/FR91/00835
FILING DATE: 23-OCT-1991
PRIOR APPLICATION NUMBER: WO PCT/FR91/00835
FILING DATE: 23-OCT-1991
PRIOR APPLICATION NUMBER: US 08/039,320
FILING DATE: 23-OCT-1993
PRIOR APPLICATION NUMBER: US 08/039,320
FILING DATE: 14-MAR-1993
PRIOR APPLICATION NUMBER: US 08/403,576
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REGISTRATION NUMBER: 35,030
REGISTRATION NUMBER: 31,030
REGISTRATION NUMBER: 017753-025
TELECOMMUNICATION INFORMATION:
TELEPAN: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2035 amino acids
TYPE: amino acids
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COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Peptide
LOCATION: 128.1899
OTHER INFORMATION: /r
OTHER INFORMATION: 11
OTHER INFORMATION: 20
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CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                 FEATURE:
                                                                                                                   NAME/KEY: Peptide LOCATION: 147 OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION:
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NAME/KEY: Peptide LOCATION: 1..21 OTHER INFORMATION: OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION:
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OTHER INFORMATION:
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LOCATION:
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P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                            Peptide
144
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134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "The amino acids spanning 128 to 1899 constitute a repeated region wherein the repeat 20 amino acids, 17 of which are fixed. The number of such repeats varies from 1 to 40."
                                                                                                                                                                                                                                                                      /note= "Amino acid 144 is Y = Xaa which is the codon for Thr or Asn wherein Thr = ACT, ACC, or ACG; and Asn = AAT or AAC."
                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Amino acid 134 is X1 = Xaa Xaa Wherein Pro = CCT, Xaa Xaa Which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA, or CCG; and Ala = GCT, GCC, GCA, or GCG."
                                                                                                                      /note= "Amino acid 147 is X2 = Xaa which is the codon for Pro or Ala wherein Pro = CCT, CCC, or CCG; and Ala = GCT, GCC, GCA, or GCG."
  /note= "Amino acids 1 to 21 are a 21 amino acid precursor sequence."
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US-08-479-537A-2

Qy	Db	Qy	Ωу	Дb	QΥ	Qy Db	рb	Qy	DЬ	Qу	B :	Qγ	Оу	DЬ	Qy	Db	VΩ	рь	Qy	DЬ	Qy	рь	Ď	P VQ	Db	γQ	P Qq	Que Bes Mat	
1045	869	œ	925 821	763	869	823 703	645	779	586	733	ū	685	630 472	420	574	360	522	301	473	241	426	181		338	66	295	236 16	che try	
5 -PNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLSD 1103	-GSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSA-PDXRPXPGST 911	KPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMP	TTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQ 984	: :	-TKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKET	TTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVTITALERA TTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVTIALERA : :	VXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAH	TTPKEPAPTTPKKPAPTTPETPPPTTSEVSTP 82	× 64	APTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSD 7	XAHGVTSAPD	TTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTP 732	APDXRPXPGS 53	XAHGVTSAPDXRPXPGSTAPXAHGVTSAPUXKEXRUSI **	PEKLAPITPEKPAPITPEELAPITPEEPTPTTPEEPAPT	41	KEPAPT 5	PDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVT 3	TKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKE 521	apdxrpxpgstapxahgvtsapdxrpxpgstapxahgvtsapdxrpxpgstapxahgvts 300	PKEPAPTIKEPAPTIPKEPAPTAPKKPAPTIPKEPAPTIPKEPAPTI 472	GSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS 2	DAVE OF COLUMN AND A CONTRACT OF COLUMN AND A COLUMN AND	TTPKEPAPTTTKSAPTTPKEPAPTTKEPAPTIFARFAL 3/0	PVTRPALGSTTPPAHDVTSAP 12	PKEPTPTTPKEPA	TSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKD-LAPTSKVLAKET 294 U	5.8%; Score 424.5; DB 2; Length 2035; Similarity 23.7%; Pred. No. 3.2e-19; 5; Conservative 69; Mismatches 511; Indels 241; Gaps	

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Patent No.
                                                                                                                                                                                                                                                                                         TELEFAX: (703) 836-202
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION: APPLICANT: CHAMBO
                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/403,576
FILING DATE: 14 + MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: PH
TITLE OF INVENTION: TR
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1104
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                                      NAME/KEY:
                                                                                                       OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                       OTHER INFORMATION:
                                                                                                                                                     NAME/KEY: Peptide
LOCATION: 128..1899
                        OTHER
                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                    NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: WO PUFILING DATE: 23-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 0 FILING DATE: 04-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: United ZIP: 22313-1404
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                                                                                                                                                                                                                                                                         ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2, Application US/09083116
5. 6203795
       INFORMATION:
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                                                                                                                                                                                                                                                                     2035 amino acids
                                          Peptide
134
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LATHE, Richard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version
                                                                                                                                                                                                                         linear
                                                                                                                                                                                                        peptide
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                                                                               /note= "The amino acids spanning 128 to 1899 constitute a repeated region wherein the 20 amino acids, 17 of which are fixed. The number of repeats varies from 1 to 40."
 /note= "Amino acid 134 is x1 = Xaa Xaa which is the codon for
                                                                                                                                                                                                                                                                                                                       2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US 08/039,320
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Best Local Similarity
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OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
                                                                       586
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                                                                                                                                                                                                                                                                                 574 TPKETAP----TIPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPT
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                                                                                                                                                                                                                                                             420
                                                                                                                                                                                                                                                                                                                          360
                                                                                                                                                                                                                                                                                                                                              522 PAPTTPKEPAPTTPK----KPAPTTPKEPAPTTPK----EPAPTTTKKPAPTAPKEPAPT
                                                                                                                                                                                                                                                                                                                                                                               301 APDXRP-XPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVT
                                                                                                                                                                                                                                                                                                                                                                                                                       473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 APDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 --DNKPAPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236 TSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKD-LAPTSKVLAKPT 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 TVLTV-----VTGSGHASSTPGGEKETSATORSSVPSSTEKNAVSMTSSVLSSHS
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RPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGS--TAPXAHGVTSAP
                             KPAP--TTPK----ETAPTTPKEPAPTTP------KKPAPTTPETPPPTTSEVSTP 822
                                                                                                                                                                                       APXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRP-XPGSTAPXAHGVTSAPDXRPXPGS
                                                                                                                                                                                                                   TPKA----AAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGT-APTTLKEPAP
                                                                                                                                                                                                                                                     SAPDXRPXPGSTAPXAHGVTS----APDXRPXPGSTAPXAHGVTSAPDXRPX----PGST
                                                             PXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAP-XAHGVTSAPDX
                                                                                           KEPAPTTPKG----TAPTTLKEPAPTTP-----KKPAPKELAPTTTKGPTSTTSD 778
                                                                                                                        TAPXAHGVTSAPDXRPXPGSTAP-XAHGVTSAPDXRPXPGSTAPXAHGVTS----APDXR 585
                                                                                                                                                                   TTP----
                                                                                                                                                                                                                                                                                                                  SAPDXRPXPGSTAPXAHGYTSAPDXRPXPGSTAPXAHGYTSAPDXRPXPGSTAPXAHGYT
                                                                                                                                                                                                                                                                                                                                                                                                             TKEPSPTTPKEPAPTT--TKSAPTTTKEPAPTT----TKSAPTTPKEPSPTTTK----E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PKE--PAPTTKEP-----APTTPKEPAPTAPK----KPAPTTPKEPAPTTPKEPAPTT 472
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                                                                                                                                                        -KKPAPKELAPTTTKEPTSTTSDKPAP--TTPKGTAPTTPKEPAPTTP 732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Amino acid 144 is Y = Xaa which is the codon for Thr or Asn or ACG; and Asn = AAT or AAC."
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Pred. No. 3.2e-19;
9; Mismatches 511;
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Db Qy	pb Qy	Фр	Qу	Qу	Qу
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104 ETNICNGKPVDGLTT-LRNGTLVAFRGHYFWMLSPFSPPSPARRITEVWGIPSPID 1158	-PNSKLVEVNPKSEDAGGABGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLSD 1103	KPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPNQT :	TTTQDTTPFKITTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQ	-TKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTS : : ;	823 TTTKEPTT 1HKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAA 868 1
	1103 957	1044	984 868	924 820	868

Search completed: April 26, 2002, 16:26:07 Job time: 507 sec

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Compugen Ltd
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C194672
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S-layer protein -
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ALIGNMENTS

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R; Jany, B.H.; Gallup, M.W.; Yan, P.S.; Gum, J.R.; Kim, Y.S.; Basbaum, C.B.	A; Residues: 1916-2193 <gu4> A; Cross-references: GB:M22405; NID:g188873; PIDN:AAA36334.1; PID:g188874 A; Experimental source: intestine</gu4>	A; lite: MOLECULAR CLORING OF human intestinal mucin cDNAs. Sequence analysis and evi A; Reference number: A33532; MUID:89197956 A; Accession: B33532	R;Gun, J.R.; Byrd, J.C.; Hicks, J.W.; Toribara, N.W.; Lamport, D.T.A.; Kim, Y.S. J. Biol. Chem. 264, 6480-6487, 1989	A; Residues: 1343-1350,'L',1352-1411,'S',1413-1448,'P',1450-1503,'T',1505-1915 <tor> A; Cross-references: GB:M74027; NID:918883; PIDN:AAA59875.1; PID:9188864 A; Note: sequence inconsistent with the nucleotide translation A. Note: sequence inconsistent with the nucleotide translation</tor>	epeated arrays	A;Experimental source: colon A;Note: sequence extracted from NCBI backbone (NCBIP:116698) R;Toribara, N.W.; Gum Jr., J.R.; Culhane, P.J.; Lagace, R.E.; Hicks, J.W.: Pararsan	Conceptual translation 2: NID:al86197: DIDN:ANASO164 1.	A:Residues: 626-1895 GU2> A:Cross-references: GB:M94131; NID:9186395; PIDN:AAA59163.1; PID:9186396 A:Note: sequence extracted from NCBI backbone (NCBIP:116706) A:Accession: B45106	A;Reference number: A45106; MUID:93016075 A;Accession: A45106 A;Status: not compared with conceptual translation A;Molecule type: mRNA	A; Residues: 1-639 < GUIDA A; Residues: 1-639 < GUIDA A; Cross-references: GB:L21998 R; Gum Jr., J.R.; Hicks, J.W.; Toribara, N.W.; Rothe, E.M.; Lagace, R.E.; Kim, Y.S. J. Biol. Chem. 267, 21375-21383, 1992 A; Title: The human MUC2 intestinal mucin has cysteine-rich subdomains located bath.	C:Date: 10-Mar-1993 #sequence_revision 12-Apr-1996 #text_change 05-Nov-1999 C:Accession: A49963; A45106; B45106; A43932; B33532; A61257; PQ0328; PQ0329 R;Gum Jr., J.R.; Hicks, J.W.; Toribara, N.W.; Siddiki, B.; Kim, Y.S. J. Biol. Chem. 269, 2440-2446, 1994 A;Title: Molecular cloning of human intestinal mucin (MUC2) cDNA. Identification of the A;Reference number: A49963; MUID:94132002	RESULT 1 A43932 mucin 2 precursor, intestinal - human (fragments) N;Alternate names: mucin SMUC-41 C.Species: Homo sapiens (man)

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J. Clin. Invest. 87, 77-82, 1991
A;Title: Human bronchus and intestine express the:
A;Reference number: A61257; MUID:91086481
A;Accession: A61257
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 'T',1925-1948,'TTS',1952-1954 <JAN>
A;Experimental source: bronchus
A;Experimental source: bronchus
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A;Title: Human intestinal mucin-like protein (MLP) is homologous with rat A;Reference number: PQ0328; MUID:92198477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GDB:120203; OMIM:158370
A;Map position: 11p15.5-11p15.5
C;Superfamily: von Willebrand factor; von Willebrand factor type A repeat homology; C;Superfamily: von Willebrand factor; tandem repeat C;Keywords: 91ycoprotein; intestine; tandem repeat C;Keywords: 91ycoprotein; intestine; tandem repeat homology <VWC>
F;2766-2834/Domain: von Willebrand factor type C repeat homology <VWC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: GB: M86523
A; Experimental source: small intestine
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A; Residues: 2328-2342, 'K', 2344-2354 < XUG1>
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A; Residues: 2328-2468
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                                                                                         LVEVNP------KSEDAGG--
                                                                                                                                                APKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPNQTPNSK 1043
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                                                           KVECEPPPMPTCSNGLQPVRVEDPDGCCWHWECDCYCTGWGD-PHYVTFDGLYYSYQGNC 2344
                                                                                                                      TPSKPTPGTKPPECPDFDPPR--
                            PHVFMPEVTPDMDYLPRVPNQGIIIN 1093
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                                                                                                                           -QENETWWLCDCFM-ATCKYNNTVEIV 2285
                                                                                                ---AEGETPHMLL---
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RESULT 2
T18262
T18262
S-layer protein - Clostridium thermocellum S-layer protein - Clostridium thermocellum C; Species: Clostridium thermocellum C; Date: 15-Oct-1999 #sequence_revision 15-C; Daccession: T18262
C; Accession: T18262
R; Fujino, T.; Beguin P.; Aubert, J.P.
J. Bacteriol. 175, 1891-1899, 1993
J. Bacteriol. 175, 1891-1899, 1993
A; Molecule type: DNA
A; Residues: 1-1664 <FUJ>
A; Cross-references: EMBL: X67506;
                                                                          A; Reference number: Z18847; MUID: A; Accession: T18262
A; Status: preliminary; translated
                                                                                                                                                                          A; Title: Organization of a Clostridium thermocellum
                                                                                                                                 Z18847; MUID:93209931
          NID: g296879;
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                  PID:g296881;
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15-Oct-1999

#text_change

15-Oct-1999

Query Match

Best Local Similarity

13.0%;

Score Pred.

950;

); DB 2; 9.5e-33;

Length 1664

Matches

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c;Species: Phytophthora infestans (potato late blight agent)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C;Accession: T31108
R;Goernhardt, B.
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A:Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 PSSKKAPPPSGASQTIKSTTKRSPK-----PPNK----KKTKKVIESEEITEVKDNKKNR 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
les 367; Conserv
                                EETTYAPAEETPYEPTEETTYAPTEETTYAPTEETTYASTEETTYAPTEETTYAPAEETP
                                                                                                    YAPTEETTYAPTEETTYAPAEETPYEPTEETTYAPTEETTYAPTEETMYAPIEETTYAPT
                                                                                                                                                                        KETTYAPTEETTYASTEETTYAPTEETTYAPAEETPYEPTEETTYAPTEETTYAPTEETT
                                                                 PTTPKEPAPTTPKEP-----APTTPKGTAPT
                                                                                                                            TAPTTPKGTAPT--TLKEPAPTTPKKPAPK-ELAPT--TTKEPTSTTSDKPAPTTPKGTA
                                                                                                                                                                                                                      ----APT----
                                                                                                                                                                                                                                            PTEET--TYTPTEETTYAPTEETTYAPTEKTTYAPTEETTYAPTEETPYEPTEETTYAPT
                                                                                                                                                                                                                                                                    PAPTTPKETAPTTPKKLIPTTPEKLAPTTPEKPAPTTPEELAPT--TPEEPTPTTPEEP-
                                                                                                                                                                                                                                                                                                                                                 TTKEP----APTTPKEPAPTTPKKPAPTTPKEPAPT--TPKEPAPTTTKKPAPTAPKE 564
                                                                                                                                                                                                                                                                                                                                                                                   PTEETTYAPTEETTYAPTEETMYAPIEETTYGPTEETTYAPTEATTYAPTEETPYAPTEE
                                                                                                                                                                                                                                                                                                                                                                                                                    P-----APT-TIKSAPT-----TIKEP----APT-TIKSAPI--TPKEPSPT 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYAPTEETTYAPTEETTYAPTEETTYAPAEETPYEPTEETTYAPTEETT-YAPTEETMYA 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPAPT-TTKSAPTTPKEPAPT---TKEPAPTTPKEPAPTTTKEPAPTTTKSAPT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYAPTKETTYAPT ---EETTYASTEETTYAPTEETTYAPAEETPYEPTEET-TYAPTEET
                                                                                                                                                                                                                                                                                                                TTYEPTGETTYAPTEETTYAPTEETTYAPTEETTYAPTEETPYEPTEETTYAPTEETPYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTYAPAEETPYEPTEETTYAPTEETTYAPTEETTYAPTEETTYAPTEETTYAPAEETPYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTKEPAPTTPKEP-----APTAPKKPAPTTPKEPAPTTPKEPAPT--TTKEPSPTTPKE 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIEETTYAPTEETTYAPAEETPYEPTEETTYAPTEETTYAPTEETTYASTEETTYAPTEE 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----TPKEPAPTTPKKPAPTTPKEPAPTTPKEPTPTTPKEP--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLAPTSKYLAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAPTTPK 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YEP----TEETTYTPTEETTYAPTEETTYAPTEKTTYAPTEETTYAPTEETPYEPTEET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLPPNSDTSKETSLTVNKETTVETKETTT---TNKQTSTDGKEKTTSAKETQSIEKTSAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TKKKPTPKPPVVDEAGSGLDNGDEKVT----TPDTSTTQHNKVSTSP-KITTAKPINPRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTKSETNAPTERMHYAHIEKPCDTEVTMYAPTEETTYAPTEETTYAPTEETTYAPTEETP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSDETEAPTEGTTYVPREETTAAPSEDTTYAPREVTPYAPTEKPYDVEETTYVTEESTYA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
-APKE---LAPT--TTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.8%;
                                                                                                                                                                                                           TPKAAAPNTPKEPAPTTPKEP----APTTPKEPAPTTPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 867; DB 2;
Pred. No. 2.5e-29;
2; Mismatches 503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 April 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                     -TLKEPAPTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AP---
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                                                                                                        1010
                                                                                                                                                                          950
                                                                                                                                                                                                                                               890
                                                                                                                                                                                                                                                                               621
                                                                                                                                                                                                                                                                                                                                                                                                                                                         712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                426
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Ωу	Qу	Qy	Qy	ОУ	Дy	Qu Be	Qy 90 Db 124 Qy 95 Db 130 Qy 100 Db 136 Db 136 C; Specis C; Specis C; Access C; Access A; Refer A; Molec A; Molec A; Molec A; Cross A; Exper C; Genet A; Map p A; Intro		Db .
326 483	294 423	235 363	180 303	136 243	95 189	uery Mi lest Lo	Db 1245 TTY Db 1245 TTY Db 1245 TTY Dy 956 NKF Db 1305 PTE Db 1305 TDI Db 1365	801 1131 855	1071
6 -TTIKSAPTTPKEPAPTTTKSAPTTPKEPAPTTTKEPA	TTTKGPATP 32TTTKGPASTTPKEPTP 32TPTKGPASTTPKEPTP 32TPTKGPASTTPKEPTP 32TPTKGPATPTKGPATPTFKEPTPTFKEPTP 32TPTKGPATPTKGPATPTFKEPTPTFKEPTP 32TTTKGPATPTKGPATPTKGPATPTFKEPTPTFKEPTP 32	VKKPSAPEKKTTTNKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAE- 293 : :	GSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPI-NPRPSLPPNSDTSKETSLT	SPKP-PNKKKTKKVIESEEITEVKDNKKNRTKK-KPTPKPPVVDEA 179 	KCCPDYESFCAEVHNPTSPDSSKKAP	<pre>/ Match</pre>	KITATTOOTSTTTOOTTPKITTKTTTLAPKVTTTKKIITTTEIM	E S E	: YEPTEETTYAP

RESULT 5
T30826
T30826
nascent polypeptide-associated complex alpha chain, muscle splice form gp220 - mouse nascent polypeptide-associated complex alpha chain, muscle splice form gp220 - mouse nascent polypeptide names: alpha-NAC protein
N;Alternate names: alpha-NAC protein
C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 24-Nov-1999
C;Accession: T30826
A;Yotov, W.V.; St-Arnaud, R.
Genes Dev. 10, 1763-1772, 1996
A;Title: Differential splicing-in of a proline-rich exon converts alphaNAC into a mus A;Reference number: 220889; MUID:96312450
A;Accession: T30826
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Cross-references: LMBL:U40363; NID:91666688; PID:91666689; PIDN:AAB18732.1
C;Genetics:

A;Gene: Naca A;Map position: 10

A;Introns: 24/1; 1996/1; 2024/3; 2050/3; 2099/3; 2142/3; 2183/3 A;Note: differential splicing converts alphaNAC into a tissue-specific DNA-binding activ C;Keywords: alternative splicing; DNA binding; transcription factor 밁 Ş Š δÃ В á В Q 밁 Ş 밁 Ş 망 ş 밁 Š В Š 밁 Š 밁 밁 õ 밁 ð 밁 Ş 망 밁 Best Local Similarity 28.4%; Pamatches 313; Conservative 126; 1028 1205 1318 1265 1145 1087 -- TPPGGVTAVPPEISLPPKETPQNATPNESLAASSQKRSPKTSVPKETPPGGVTAMPLE 1144 1376 896 916 211 805 746 SPT-PPSSKGAPVPSTGAPPSPKGAPIVPTESSISSKQVPAEILPSPQKTPEVTASRLIS 804 409 373 323 263 856 PVAPSNEATIVPTEIPTSLKNALAAATPKETLATSIPKVTSPSPQKTPKSVSLKGAPAMT 156 EVKDNKKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNK-----VSTSPKIT 109 NPTSPPSSKKAPPPS-GASQTIKS-----TTKRSPKP--PNKKKTKKVIESEEIT TAKPINPRPSLPPNSDTSKETSL--TVNKET----TVETKETTTTNKQTSTDGKEKTT AVQSPKVDPIMSDVTPTSPKKTSA-----TAVPKDTSATLSLKSVPAVTSLSPPKA GVPVTLTPKGAPNALAE-SPASPKKVPKTAAPEETSTTP-----SPQKIPKVAGPKEAS 1317 PSPTTTKEPAPTTPKEPAPTTPKKPAPTT--PKE-------PAPTTPKEPAP--- 551 IPSAPQKAPKTAVPKQIPTPEDAVTILAGSPLSPKKASKTAAPKEAPATPSVGVIAVSGE 1204 APTTPKEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTT--PKEPAP----TTPKE 462 SSSKRAPKTAVSKEIPSKGVTAVPLEISLPLKETSKSATPGEKSASSPKRSPKTAGPKE- 1086 GPPATLAETPTYPKKSPKPAASKKTPATPSPEGVTAVPLEIPPCSKKAPKTAAPKESSAT 1027 PTPTTIKSAPTTPKE-PAPTTTKSAPTTPK-----EPAPTTTKEPAPTTPKEPAPT 372 SKKAT---EIAASKDVSPSQ--FPKEVPLLQHV---PPTSPPKSPVSDTLSGALTSPPPK SAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKE 322 KLSQTVGPKETSLEGATAVPLEIPPSHKKAPKTVDPKQVPLTPSPK-DAPTTLAE-SPSS 1492 PVQIPPSPRKGSKKAGSKE-TPTTPSPEGVTAAPLEIPISSKKTSKMASPKETLVTPSSK 1434 PKETAPTTPKGTAPTTLKEPAPTTP-------KKPAPKELAPTTTKE 697 ATPPSKKTPKTAVPKETSAPSEGVTAVPLEIPPSPRKAPKTAAPKETPAPS--PEGATTA 1375 PTTPEEPTPTT-----PEEPAPTTPKAAAPNTPKEPAPTTPKE-PAPTTPKEPAPTT 657 ---TTTKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEK-PAPTTPEELA 606 ISPSPKKTSKTAAPKENSATLPPKRSPKTAAPKETPATSSEGVTAVPSEISPSPPTPASK 1264 PAPTTTKEPSPTTPK-----EPAPTTTKSAPTTTKEPAPTTT-KSAPTTPK-----E 508 --PPTTSEVSTPTTTK-----EPTTIHKSPDESTPELSAEPTPKALENSPKE-PGVPTT 858 PKK-APKTAAPPSER-VTTVPPEKPA-TPQKASGTTASKVPVPAETQEVAVSSRETPVTP PKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPTTPETP---PTS----TTSDKPAPTTPKGTAPTTPKEPAPTTPKE-PAPTTPKGTAPTTLKEPAPTT 750 11.3%; Score 828.5; DB 2; Pred. No. 1.5e-27; Mismatches 436; Length 2187; Indels 229; Gaps 915 262 855 155 967 52;

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1608 K-PVTT--SLAQTAPPSLQKAPSTTIPKENLAAPAV----LPVSSKSPAAPARASASLSP 1660

밁

861 TPKPASPPAHVSSPPEVVKPSTP--PAPTTVISP-PSEPKSSPPPTPVSLPPPIVKSSPP 917

KTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVT

	QY 593 TPEKPAPTTPEELAPTTPEEPTTTPEEPAPTTPKAAAPNTPKE-PAPTTPKEPA 646	
	Db 801 SPPLAPVSSPPQVEKTSPPPAPLSSPPLAPKSSPPHVVVSSPPPVVKSSPPPAPVSSPPL 860	
	Qy 541 PAPTTPKEPAPTTTKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPT 592	
	TTTKSAPTTTKEPAPTTTKSAPTTPKEPSP	
	693 IPSPPPQEKPTPPSTPSKP-PSSPEKPSPPKEPVSSPPQTPKSSPPPAPVSSPP 74	
	Qy 421 PKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPA 480	
	633 PPPMKSPPPPTPVSSPPPPE	
	KKPAPTTPKEPAPTTPKEPTP	
	Db 575 PPPPVKSPPPPTLVASPPPPVKSPPPPAPVASPPPPVKSPPPPTPVASPPPPAPVASS 632	
	PKEPTPTTIKSAPTTPKEPAPTTTKSAPTTPKEPAPTTTKEPAPTTPKEP	
	Db 519 PVKTTSPPAPIGSPSPPPPPVSVVSPPPPPVKSPPPPAPVGSPPPPEKSPPPPAPVAS 574	
	AKPTPKAETT	
	Db 484 ATSPSPQVQPPAASTPPPSLVKLSPPQAPVGSPPP 518	
	TTAKPINPRPSLPPN	
	Db 440VSPEPLPEPSPVPAPAPMPMPTPHSPPAD	
	QY 142 KKKTKKVIESEEITEVKDNKKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHN 201	
	QY 82 RECDCDAQCKKYDKCCPDYESFCAEVHNPTSPPSSKKAPPPSGASQTIKSTTKRSPKPPN 141	
36;	Query Match 10.9%; Score 800; DB 2; Length 1188; Best Local Similarity 28.7%; Pred. No. 1.3e-26; Matches 246; Conservative 64; Mismatches 401; Indels 146; Gaps	
	Accession: S499; Status: prelimit Molecule type: I Residues: 1-1188; Cross-references	
	Rubinstein bmitted to Descriptio Reference	
	RESULT 6 \$49915 \$49915 C:Species: Lea mays (maize) C:Species: Lea mays (maize) C:Date: O5-Mar-1995 #sequence_revision 12-May-1995 #text_change 29-Oct-1999 C:Accession: \$49915	
	Qy 1039 TPNSKLYEVNPKSEDAGGAEGETP 1062 : ::	
	Db 1717PKKASSSKRASTLPATTLPSLKEASVLSPTA 1747	
	RVRKPKTTPTPRKMTSTMPELNPTS	
	SITUATIVE TERMINIST STANDARD TO STANDA	
	Ov 919 STTTOOTTOTKTTTTKTTTAKKUTTTKKTTTTKTTKKTTTTKKKKKKKK	

Query Match Best Local

hes 318;

Similarity

10.9%;

Conservative

Indels Length

51;

```
RESULT 7
$348478
glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - yeast (Saccharomyces cerevisiae)
N;Alternate names: extracellular glucoamylase; mucin-like protein MCC1; protein
C;Species: Saccharomyces cerevisiae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 12-Nov-1999
C;Accession $48478; A26877; B26877; S27281; JC6123
R;Rowley, K.
submitted to the EMBL Data Library, October 1994
A:Reference number: $48478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: S48478
A; Accession: S48478
A; Molecule type: DNA
A; Residues: 1-1367 <ROW>
A; Cross references: GB: 247047;
A; Cross references: GB: 247047;
C;Superfamily: yeast glucan 1,4-alpha-glucosidase homolog; gluco;Keywords: glycosidase; hydrolase; polysaccharide degradation; F;5-21/Domain: transmembrane #status predicted <TM1> F;1350-1366/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                      A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residus: 1-1367 <LAM>
A;Cross-references: GB:U30626; NID:g1304386;
                                                                                                                                                                                                                                                                             A; Residues: 1-31 < PAR>
A; Cross-references: EMBL:X13857; NID:g4551; PR; Lambrechts, M.G.; Bauer, F.F.; Marmur, 51; Proc. Natl. Acad. Sci. U.S.A. 93, 8419-8424; A; Title: Mucl, a mucin-like protein that is rA; Reference number: JC6123; MUID:96323237
                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Similar short elements
A; Reference number: S27281; MUII
A; Accession: S27281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:M16165; NID:g172523; PIDN:AAA35015.1; R;Pardo, J.M.; Tanez, E.; Zalacain, M.; Claros, M.G.; Jimenez, FEBS Lett. 239, 179-184, 1988
                                                                                     A; Map position:
                                                                                                         A; Cross-references: MIPS: YIR019c;
                                                                                                                                A; Gene: SGD: MUC1; STA2;
                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-31 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 762-1331 <YA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: EMBL:M16164; A; Accession: B26877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-242 < YAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Yamashita, I.; Nakamura, M.; Fuk
J. Bacteriol. 169, 2142-2149, 1987
A;Title: Gene fusion is a possible
A;Reference number: A91831; MUID:8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δÃ
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                                                                                                                                                                                                                                                                A; Accession: JC6123
                                                                                                                                                      Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1142 PAPPKKEEQSLPPPAES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSSPP----PPVKSPPPPAPVSSPPPPVKSPPPPAPISSPPPPVKSPPPPAPVS---SPPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VKSPPPPAPVSSPPPPIKSPPPPAPVSSPPPAP-----VKPPSLP-PPAPVSSPPPVVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAMVSSP-PMTPKSSPPPVVVSSPPPTVKSSPPPAPVSSPPATPKSSPPPAPVNLPPPEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAATKPEMTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KKPAPKELAPTTTKGPTSTTSDKPAPT-TPKETAPTTPKEPAPTTPKKPAPTTPETPPPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KSSPPPTPVSSPPPA---PKSSPPPAPMSSPPPPEVKSPPPPAPVSSPPPPVKSPPPPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KE---PTSTTSDKPAPTTPKGTAPTTP-KEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTTPKEPAPTTPKETAPTTPKGTAPTTLKE---PA----PTTPKK---PAPKELAPTTT
                                                                                       9R
                                                                                                                                MAL5; DEX2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        possible mechanism
l; MUID:87194600
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CCI 9.98; SCOTE (04.5; DB 2; Length 1151; al Similarity 25.78; Pred. No. 1.2e-722; 304; Conservative 104; Mismatches 445; Indels 331; Gaps AEVHNPTSPPSSKKAPPPSG	udery ma Best Loc Matches 105 39 141	D 04 D 04 Z 20
en - chicken (fragment)) ision 15-Oct-1999 #text_change 15-Oct-199 , S. , S. ted high molecular mass nuclear antigen, 9803440 from GB/EMBL/DDBJ NID:d1177138; PID:d1025045; PIDN:BAA24137	Q: ::270 V 3Q	PAPAPAGE COCHER
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   VRKPKTTPTPRKMTSTMPELN-
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                                                                                                                      KTTESKITATTTQ-VTST----TTQDTTPFKITTLKTTTLAPKVT---TTKKTITTTEIMN
                                                                                                                                                                                                                                                                           EVTTTEKEKVVQTTPITTEKSTTQEETTTTTTTTEKTTSKTTTEKPTTSESATTETTTSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KAPATTEEPTPTTTEE--VTTTEAETSTTTSSETSTEK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKA
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                                                                                         TTSAVAASTTTTEPITTTEKSTTLETTPIEATTLNEVTGPAFVTGAPVDETTINTLELLS
                                                                                                                                                                                                                                            PTTIHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDLR
                                                                                                                                                                                                                                                                                                       --TSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPTTPE--TPPPTTSE-VSTPTTTKE
                                                                                                                                                                                                                                                                                                                                       VVESSTPRQLPERWKAIVNKFKHNLEVLKEKKRLLKEKESTSTTGSDSSETTTVVAENID
                                                                                                                                                                                                                                                                                                                                                                                                 --GSTTTEEPTTTAIFAEASTGIITTDEETTSTTSTTPEITSTKE--IVTESAITQTSVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STAESTTTALPFTTEQTVTTEEPTTAEKSTATQ----KPTTTQESVST--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEAKENDDYNHLDYNHYREAKEPTTTEESSTTEEVTTTEEPANTGNPPTTENPTTTEQPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----TSTDASTTNAPTTGKDSTTPEIITGIVVINSKSESVTDMSTTRFSTTLSPTTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNGDFKVTTPDTSTTQ---HNKVSTSPKITTA-KPINPRPSLPPNSDT--
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                                                                                                                                                    -TSETTTSESAAFITGESPENTALQSSSQKSEENESSAEKPGARRDFVPKKHKTTVKPAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PSPTTPKEPAPTTKSAP-----
                               -INNTQISQPKPTDISKTDALSSLISGLIGSFTKAPMAPTI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -PAPTTPKEPAP ----TTTKKPAPTA--PKEPAPTT---PK
                                                                                                                                                                                                                                                                                                                                                                                                                   -TTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                         -ESSTIGKATIPELSTISEETITIELKITIE-----
                                                                                                                                                                                                                                                                                                                                                                   KKPAPKELAPTTTKGP----
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                                                                                                                                                                                                                -TVDTSSATTEESSTAAETTTTSAE--
                                                           -KPTKAPKKPTSTKKPKTMPR
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                                                                                                                                                                                    -APKMTKETATTTE
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뮍 1023 ----HTTTDAAFVTATEASLNDGSDKKIIDEAQPTDEIRRA 1059

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Biochem. Biophys. Res. Commun. 165, 644-649, 19 A; Title: Sequence analysis of the 5' region of A; Reference number: A36735; MUID:90088473 A; Accession: A36735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:J05581; NID:g188669; PIDN:AAA59
A;Note: GenBank entry HUMMUCAB includes one copy of th
R;Lan, M.S.; Batta, S.K.; Qi, W.N.; Metzgar, R.S.; Hol
J. Biol. Chem. 265, 15294-15299, 1990
A;Title: Cloning and sequencing of a human pancreatic
A;Reference number: A35887; MUID:90368716
A;Accession: A35887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Gendler, S.J.; Lancaster, C.A.; Taylor-I
J. Biol. Chem. 265, 15286-15293, 1990
A;Title: Molecular cloning and expression
A;Reference number: A35886; MUID:90368715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-19,29-952,1033-1344 <LIG2>
A; Residues: 1-19,29-952,1033-1344 <LIG2>
A; Cross-references: GB:M32739; GB:J05288; NID:g182126; PIDN:AAA3580
A; Cross-references: Splice form B
A; Note: GenBank entries HUMEPISIB1 and HUMEPISIB2 present only the
A; Note: GenBank entries HUMEPISIB1 and HUMEPISIB2 present only the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-952,1033-1344 <LIG1>
A;Residues: 1-952,1033-1344 <LIG1>
A;Cross-references: GB:M32738; GB:J05288; NID:g182121; PIDN:AAA35804.1; PID:g182124;
A;Cross-references: GB:M32738; GB:J05288; NID:g182121; PIDN:AAA35804.1; PID:g182124;
A;Cross-rimental source: splice form A
A;Note: GenBank entries HUMEPISIAl and HUMEPISIA2 present only the amino-and carboxyl
A;Accession: B35175
                                                            A; Molecule type: mRNA
A; Residues: 1-142, 'Q'
                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-19,29-155,'p',157-175,'p',177-182,'A',184-212,1033-1037,'A',
A;Cross-references: EMBL:X52229; NID:g37053; PIDN:CAA36478.1; PID:g37054
R;Abe, M.; Siddiqui, J.; Kufe, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-19, 29-155, 'P', 157-175, 'P', 177-182,
A; Cross-references: EMBL: X52229; NID: g37053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Human epithelial tumor antigen cDNA sequences. A;Reference number: S10571; MUID:90276413 A;Accession: S10572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-19, 29-1109, '8', 1111-1339, 'A', 1341-1344 < LAN>
A; Residues: 1-19, 29-1109, '8', 1111-1339, 'A', 1341-1344 < LAN>
A; ROSS-references: GB: J05582; NID: g18598; PIDN: AAA60019.1;
A; NOTE: GenBank entry HUMPANNU Commanifetty T. Smorrodinsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Ligtenberg, M.J.L.; Vos, H.L.; Gennissen, A.M.C
J. Blol. Chem. 265, 5573-5578, 199.
A;Title: Episialin, a carcinoma associated mucin,
A;Reference number: A35175; MUID:90202794
                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: S40293
A; Accession: S40293
                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Wreschner, D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-19,29-992,1033-1344 <GEN>
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C;Accession: A35175; B35175; A35886; A35887; S10572; S40293; A36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Species: Homo sapiens (man)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: not compared with conceptual translation
Residues: I-142,'Q',144-162,'Q',164-168 <ABE>;Cross-references: EMBL:M31823; NID:g181542; PIDN:AAA35757.1; Masuzawa, Y.; Miyauchi, T.; Hamanoue, M.; Ando, S.; Yoshida,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Biochem. 189, 463-473, 1990
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J.
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      PID:g181543
J.; Takao,
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sequence

N.; Burc

epith

S10218

episia

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Shimazu

1039-1344

repeated se; Zaretsky,

may

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A; Note: undetermined tyrosine residues in the carboxyl-terminal non-repetitive region at C; Comment: This protein is length polymorphic. Individuals may have between 21 and 125 c partial repeats. The repeat shown is defined by SmaI nuclease sites.

C; Comment: Serine and threonine residues in the tandem repeat domain are extensively gly C; Comment: For an alternative splice form without a tandem repeat domain, see PIR:S48146 C; Genetics:

A; Gene: GDB:MUC1; PUM
A; Cross-references: GDB:120705; OMIM:158340
A; Map position: 1q21-1q23
A; Introns: 20/1; 62/3; 1165/3; 1184/2; 1230/1; 1270/3; 1320/3
C; Superfamily: polymorphic epithelial mucin
C; Keywords: alternative splicing; duplication; glycoprotein; phosphoprotein; polymorphis F; 1-13/40/Product: mucin 1 precursor, splice form A #status predicted <PREA>
F; 1-23/Domain: signal sequence #link PREA #status predicted <SIGA>
F; 1-19,29-32/Domain: signal sequence #link PREA #status predicted <SIGB>
F; 1-19,29-1344/Product: mucin 1 precursor, splice form B #status predicted <PREB>
F; 1-19,29-1344/Product: mucin 1 precursor, splice form B #status predicted <PREB>
F; 1-19,29-137/Domain: corboxyl-terminal non-repetitive
F; 1245-1272/Domain: transmembrane #status predicted <PREB>
F; 1143-1344/Region: mucin 1 carboxyl-terminal non-repetitive
F; 1245-1272/Domain: transmembrane #status predicted <PREB>
F; 1213/Binding site: phosphate (Tyr) (covalent) #status predicted
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A; Title: A novel core protein as well as polymorphic epithelial mucin carry peanut agglu A; Reference number: JX0235; MUID:93123189
A; Accession: PX0066
A; Molecule type: mRNA
A; Residues: 998-1011, 'ES', 1014-1017;1018-1032, 'T', 1034-1037;1038-1057 <MAS>
A; Residues: 998-1011, 'ES', 1014-1017;1018-1032, 'T', 1034-1037;1038-1057 <MAS>
A; Experimental source: gastric carcinoma cell
A; Elroy-Stein, O.; Keydar, I.; Wreschner, D.H.
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R. Zrihan Licht, S.; Barucu, ...
FEBS Lett. 356, 130-136, 1994
A. Title: Tyrosine phosphorylation of the MUC1
A. Treamer number: S51026; MUID:95080414
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                                                                                                        T-SAPDT--RPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPA
                                                                                                                                                                TKSAPTTPKEPSPTTTKEP-----APTTPKEPAPTTPK----KPAPTTPKEPAPTTPK-
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elastic titin - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision
C;Accession: I38346
R;Labeit, S; Kolmerer, B.
Science 270, 293-296, 1995
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                                                                                                                                                                        A;Cross-references:
A;Map position: 2q31
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C;Genetics:
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  7819 VGSSAIFECLVSPST 7833
                                    1020 NPTSRIAEAMLQTTT 1034
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                                                                                                                                                                                                                                                                                                                            7611 KVPGGEKKVRKLLPERKPEPKEEVVLKSVLRKRPEEEEPKVE----PKKLE-KVKKPAVP 7665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              641 TPKEP-----APTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTT 694
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                                                                                                                                                                                                                                                                                                                                                                TPPPTTSEVS--TPTTTKEP-----TTIHKSPDESTPELSAEPTPKALENSPKEPGVP 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VPKKPEVPPAKVPEVPKKPV----LEEKPAVP----VPERAESPPPEVYEE--PEEIAP-- 7499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --PKKPEVTPVK-VPEAPKEVVPEKKVPVP-PPKKPEVPPTK-----VPEVPKVAVPEKK 7336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PKEPAPTTKEPAPTTP------KEPAPTAPKKPAPTTPKEPAPTTTKEPSP 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EKKVPVPPAKKPEAP----PPKVPEAPKEVVPEKKVPVPPPKKPEVPPTKVPEVPKAAV 7226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TPKEPAPTTTKEPAPTTTKSAPTTPKEPAPTTPKK----PAPTTPKEPAPTTPKEPTPTT 420
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                                                                                PIKGVPKKTPSPIEAERRKLRPGSGGEKPPDEAPFTYQLKAVPLKFVKEIKDIILTESEF 7818
                                                                                                                    RATNSKATTPKPQKPTKAPKKPTS--TKKPKTMPRVRKPKTTPTP-----RKMTSTMPEL 1019
                                                                                                                                                                                                     TTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNK-----PEETAKPKD 966
                                                                                                                                                                                                                                         ---EPPPPKPVEEVEVPTVTKRERKIPEPTKVPEIKPAIPLPAPEPKPKPEA------
                                                                                                                                                                                                                                                                                 TTKTPAATKP----EMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITA 912
                                                                                                                                                                                                                                                                                                                                                                                                        EPEKV---IEKPKLKPRPPPPPPPPPPPPKEDVKEKIFQLKAIPKKKVPENPQVPEKVELTPL 7610
                                                                                                                                                                                                                                                                                                                                                                                                                                          APKELAPTTTKGPTSTTSDKPAPTTPKETA-----PTTPKEPAPTTPKKP--APTTPE 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -EEEIAPEEEKPVPVAEE----EEPEVPPPAVPEEPKKIIPEKKVP-VIKKPEAPPPKEP 7553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKP 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APAVVAKKPELPPVKVPEVPKEVVPEKKVPLVVPKK--PEAPPAKVPEVPKEVVPEKKVA 7450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APTT----PEKPAPTTPEELAPTTPEEPTP-TTPEEPAPTTPKAAAPNTPKEPAP----T 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VP----EAIPPKPESPPPEVFEEPEEVALEEPPAEVVEEPEPAAPPQVTVPPKNPVPEKK 7392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEKKVPEAIPPKPESPPPEVFEEPEESPSAPPK-KPEVPPVRVPEVPKEVVPEKKVPAAP 7285
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                                                                                                                                                            -----EVKTIKPPPVEPEPTPIAAPVTVPVVGKKAEAKAPKEEAAKPKG 7758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----DLAPTSKVLAKPTPKAETTTKGPALT----TPKE 306
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Qy 145 Db 1950 Qy 205 Db 1992 Qy 261 Db 2052 Qy 317 Db 2111 Qy 376 Db 2170 Qy 434 Db 2230 Qy 492 Db 2341 Db 2341 Qy 575	Query Ma Best Loc Matches Qy 27 Db 1781 Qy 68 Db 1836 Qy 90 Db 1896	RESULT 12 T34513 T34513 hypothetical prote: C; Species: Caenorhe C; Species: 29-Oct-1999 C; Accession: T34511 R; Favello, A.; Vau submitted to the El A; Description: The A; Reference number A; Reference number A; Recassion: T34511 A; Status: prelimina A; Molecule type: Dl A; Residues: 1-3507 A; Cross-references A; Experimental sou C; Genetics: A; Map position: 3 A; Map position: 3 A; Introns: 14/1; 44
TKKVIESEEITEVKDNKKNRTKKKPTPKPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVS 204	Match 9.1%; Score 668; DB 2; Length 3507;	RESULT 12 T34513 hypothetical protein ZK783.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Caete: 29-Oct-1999 #text_change 29-Oct-1999 C;Accession: T3451 R;Favello, A.; Vaudin, M. Submitted to the EMBL Data Library, August 1994 A;Description: The sequence of C. elegans cosmid ZK783. A;Description: The sequence of C. elegans cosmid ZK783. A;Cession: T34513 A;Accession:

2457

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2516 327

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R;Desseyn, J.L.; Guyonnet-Duperat, V.; Porchet, N.; Aubert, J.P.; Laine, A.
J. Blol. Chem. 272, 3168-3178, 1997
A;Title: Human mucin gene MUC5B, the 10.7 kb large central exon encodes various A;Reference number: Z22899; MUID:97166151
A;Accession: T45025
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-3570 <DES>
A;Cross-references: EMBL:Z72496; NID:g1834502; PIDN:CAA96577.1; PID:g1834503
A;Experimental source: placenta
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745025
mucin MUC5B, tracheobronchial [imported] - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_ch
C:Accession: 745025
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    168
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                                                                                                                                       y Match 9.1%; Score 663; DB 2;
Local Similarity 26.1%; Pred. No. 1.9e-20;
hes 322; Conservative 92; Mismatches 489
                                                                                                                                                                                                                                                                                                   MUC5B
KPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAK-----PINPRP
                                  STPATSSTATPSSTPGTTWILTKLTT-----TATTTESTGSTATPSS-----
                                                                                                                VECSLDFGLVC-----RNRE----QVGKF-KMCFNYEIRVFCCNYGHCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAP----PPPSNGGYGEETNQEEEQVTSTTT
                                                                         TSPPSSKKAPPPSGASQT---IKSTTKRSPKPPNKKKTKKVIESEEITEVKDNKKNRTKK
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            1033 TTRPNQ--TPNSKLVEVNPKSEDAGGAEGETPH
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                                                                                                                                                                                                                                                                                                                                                                TPHVSTT-ATTPTVTSSKATPSSSPGTATALPALRSTATTPTATSFT----AIPSSSLGT
                                                                                                                               TTTTTTVATGSMATPSSSTQTSGTPPSLTTTATTITATGSTTNPSSTPGTTPIPPVLTSM
                                                                                                                                                                    TLKTTTLA----AKPKDRATNSK
                                                                                                                                                                                                          VPTTTTTGFTATPSSSPGTALTPPVWISTTTTPTTTTTTTSGSTVTPSSIPGTTHTARVL
                                                                                                                                                                                                                                                                                                                                                                                             TPPPTTSEVSTPTTTKEPTTIHKSPDEST--PEL-SAEPTPKALENSPKEPGVPT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                              TWILTELTTTATTTASTGSTATLSSTPGTTWILTEPSTTATVTAPPGSTATASSTQATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -PKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTP-EEPAPTTPKAAAPNTPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --TQGPP----AG-----TPHVSTT-----TTPTVTSKATPFSSPGTATALP
                                                   ATT----PAATSSKATSSSSPRTATTL--PVLTSTATKSTATSFTPIPSS----TLWTT
                                                                                        ATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQT 1032
                                                                                                                                                                                                                                                                                      TWIRLSQTTIPTATMSTATPSSTPETVHTSTVLTTTATTTGATGSVATPSSTPGTAHTTK
                                                                                                                                                                                                                                                                                                               -----TKTPAATKPEMTTTAKDKT--TERDLRTTPETT-----TAAPKMTKETATTTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -TATTLPVLTSTATKSTATSVTP-----IPSSTLGTTGTLPEQTTTPVATMSTIHPSST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTNPSSTPGTTPIPPELTTTATTPAATSSTVTPSSALGTTHTPPVPNT--TATTHGRSLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PKKPAPKELAPTTT--KGPTSTTSDKPAPT---TPKETAPTTPKEPAPTTPKKPAPTTPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ILTELTTT-----ATTTASTGSTATPSSTPGTAPPPKVLTSPATTPTATSSKATSSSSPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EPAPTTPK-----EPAPT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EPQCAWSEWLDYSYPMPGPSGGDFDTYSNIRAAGGAVCEQPLGLECRATAQPGVPLGELG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AKDLAPTSKVLAKP--TPKAETTTKGPALTT----PKEPTPTTPKEPASTTPKEPTPTT
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972 3268 3208

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3148

857

3093 805 3033 750 2973 695

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nucleolar phosphoprotein - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 24-Sep-1999
C;Accession: I51618; S57757
R;Cairns, C.; McStay, B.
J, Cell Sci. 108, 3339-3347, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Superfamily: nucleolus-cytoplasm shuttle phosphoprotein C; Keywords: phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Identification and cDNA cloning of a Xenopus nucleolar phosphoprotein, xNopp180; Reference number: I51618; MUID:96019267 A;Accession: I51618 A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-990 <CAI>
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Best Local Similarity 25.8%;
Matches 260; Conservative 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                    DSSDEEEQPAKKAKIVPAKAAASAPKPLAKKAETSTDSESDSSSEDEKKSSVKLGVKAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GKKSSSREDSSDSSDEEQKTAKSKPKPDVYSAVPPPTSVSKKKTLSQPGTKAKPESSDSS
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  STTSDKPAPTTPKGTAPTTPKEPAPTT--PKEPAPTTPKGTAPTTLKEPAPTTPKKPAPK 757
                                      SSSDSSDSSEDEKKSSAKPAVKTTPGKATS-----KPVVASKPVPAK-----KASS
                                                                           TPKEPAPTTPKEPAPTTPKETAPTTP-KGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPT
                                                                                                                                                          PEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPTTP-KAAAPNTPKEPAPT----
                                                                                                                                                                                                 KSAATPTSKTP---TNSKATPTSKKTPAKPGTPKTSAAKKDSSSSDSSSSSSEKKTPA-
                                                                                                                                                                                                                                     EPAPT-TPKEPAPTTTKKPAPTAPKEPA-PTTPKETA--
                                                                                                                                                                                                                                                                            TSKTPTNGK---ATPTSKTPAKPGTPKTSTAKKDSSSSDSSDSSDEETTTKPAAKTTPA 473
                                                                                                                                                                                                                                                                                                                TKSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKEPAPTTPKEPA----PTTPKKPAPTTPK 539
                                                                                                                                                                                                                                                                                                                                                       KK-APAAP--DAKSTPVAAAKKSAPAKKASSSSDSDSSSNEETTTKPAAKTTPAKSAATP 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----TPKKPAPTTPKEPAPTTP----KEPTPTTPKEPAPTTKEPAPTTPKEPAPTAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPKAETTTKGPALTTPKEPTPTTPKE----PASTTPKEPTPTTIKSAPTTPKEPAPTTTK 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KETSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKVLAKP 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PKPPVVDEAGSGLDNGDFKVTTPD--TSTTQHNKVSTSPKITTAKPINPRPSLPPNSDTS
                                                                                                                   -KRAAKTTPAKPA-----AKTTPAKPA-----AKTTPAKPAAKSTPGKQVPTKKES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----VAAVKTPTQKKAKS-----SSSESSSEDEASKKKQPVIKV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 646; DB 2; Length 99
Pred. No. 2.9e-20;
34; Mismatches 389; Indels
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                        142 YKSPPPPSPSPPPPYVYKSPPPPSPSPPPPYYYKSPP--
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807 PPPTTSEVSTPTTTKS-PTTTKKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAATK 66 1	Db 622 SSDSDSSEEETTKTTK Qy 758 ELAPTTTKGP Db 679 SATPVNTKAPAQNKAS	SDSDSSEEETTKTTKPLTKLSPAVKTLPPKKAESSSDSSDSEKKTKPAKPPAK 678 LAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEDAPTTPKK-PAPTTPET 806 LAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEDAPTTPKK-PAPTTPET 806 ATPVNTKAPAQNKASKASCSDSDSSSEEEGKSKQPTGKSPAAKATAPPKKNPVAVNKDK 738
QAAAAKDVKQGAKAAKPTPKKAASSSSEDSSSDEDVSK 79 PPETTTAADKMTKETATTTEXTTEXTTTTOUTSTTTQDT 92 : : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::	807 PPPTTSEVS	PTTIHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAATK 8
PRETTTAAPKMTKETATTTEKTTESKITATTTQVTSITTQDT 92 PRACKESSSESSDSEDEKQGGKNTSTTKIANST 84 PRAVPAAKKESSSESDEEDEKQGGKNTSTTKIANST 84 PRAVPAAKKESSSESDEEDEKQGGKNTSTTKIANST 84 PTTKKTITTTEIMNKDEETA-KPKDRATNS	739 PSSSSSSDS	SSSEDSSSDEDVSK 7
FFRAVPÄAKKESSESSDSEDEKQGGKNTSTTKIANST 84 FFRAVPÄAKKESSESSDSEDEKQGGKNTSTTKIANST 84 FFRAVPÄAKKESSSESDSEDEKQGGKNTSTTKIANST 84 FFRAVRETTPTEIMNKPEETA-KPKDRATNSKATTPKPQ 97 :	866 P	ESKITATTTQVTSTTTQDT 9
ABCSSESSSEDEGKANGTSGKRKRESTGNAECEAVTPE 89 RVRKPKTTPTP-RKMTSTMPELNPTSRIAE 1027	796 AKKTNTAVSKSPV-	-TTPKAVPAAKKESSSESSDSEDEKQGGKNTSTTKIANST 8
ABCCSESSSEDEGKANGTSGKRKRESTGNAECEAVTPE 89 PRVRKPKTTPTP-RKMTSTMPELLPTSRIAE 1027	926 TPFKITTLKTTTLA	-KTITTTEIMNKPEETA-KPKDRATNSKATTPKPQ
COWPEA	848	SSSEDEGKANGTSGKRKRESTGNAECEAVTPE 8
COWPEA (COWPEA) (COWP	980 K	-RKMTSTMPELNPTSRIAE 102
Cowpea) (cowpea) (cow	RESULT 15	
Broughton, W.J.; Krause, A. 10, 95-101, 1997 10, 95-101, 1997 10, 95-101, 1997 20t-hair-specific expression of extensin gene dUD:97155574 lated from GB/EMBL/DDBJ lated f	extensin class 1 precurso C; Species: Vigna unguicul C; Date: 16-Jul-1999 #sequ C; Accession: T11622; S541	cowpea (cowpea) e_revision 16-Jul-1999 #text_change 17-Nov-2
lated from GB/EMBL/DDBJ 336; NID:g1015936; PIDN:CAA62943.1; PID:g1015 pecies Red calcona Broughton, W.J; Krause, A. Broughton, W.J; Krause, A. brary, April 1935 5t-hair specific extensins involved in rhizob 1 core fice extensins involved in rhizob 1 core fice extensins involved in rhizob 2 core fice extensins involved in rhizob 2 core fice extensins involved in rhizob 2 core fice extensins involved in rhizob 3 core fice extensins involved in rhizob 2 core fice extensins involved in rhizob 3 core fice extensins involved in rhizob 4 core fice extensins involved in rhizob 3 core fice extensins involved in rhizob 3 core fice extensins involved in rhizob 4 core fice extensins involved in rhizob 3 core fice extensins involved in rhizob 4 core fice extensins involved in rhizob 5 core fice extensins involved in rhizob 6 core fice extensin	R; Arsenijevic-Maksimovic, Mol. Plant Microbe Intera A; Title: Rhizobia modulat A; Reference number: Z173	: Broughton, W.J.; Krause, A. 10, 95-101, 1997 oot-hair-specific expression of extensin gen MOID:97155574
336; NID:g1015936; PIDN:CAA62943.1; PID:g1015 pecies Red caloona ; Broughton, W.J.; Krause, A. bbrary, April 1995 pt-hair specific extensins involved in rhizob pt-hair specific extensins involved in rhizob pt-hair specific extensins involved in rhizob pt-rich glycoprotein froxyproline pe #status predicted <sig> pe #status predicted <mat> lass 1 #status predicted <mat> lass 1 #status predicted <mat> ass 1 #status predicted <mat> bass 1 #status predicted <mat> ass 1 #status predicted <mat> ass 1 #status predicted <mat> bass 1 #status predicted <mat> ass 1 #status predicted <mat> ass 1 #status predicted <mat> bass 1 #status predicted <mat> ass 1 #status predicted <mat> ass 1 #status predicted <mat> bass 1 #status predicted <mat> ass 1 #status predicted <math #status="" 1="" <math="" ass="" pred<="" predicted="" status="" td=""><td>A; Status: preliminary; tr A; Status: preliminary; tr A; Molecule type: DNA A; Residues: 1-489 < ARS></td><td>lated from GB/EMBL/DDBJ</td></math></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></mat></sig>	A; Status: preliminary; tr A; Status: preliminary; tr A; Molecule type: DNA A; Residues: 1-489 < ARS>	lated from GB/EMBL/DDBJ
Dibrary, April 1995 Dibrar	A; Experimental source: su R; Arsenijevic-Maksimovic,	ecies Red Callona Broughton, W.J., Krause, A.
330; NID:g791149; PID:g791150 =:rich glycoprotein iroxyproline = #status predicted <sig> = #status predicted <mat> lass 1 #status predicted <mat> - 2%; Pred. No. 5.2e-20; - 1 </mat></mat></sig>	A; Description: A class of A; Reference number: S5415 A; Accession: S54155	ot-hair specific extensins involved in rhiz
PAPTITKEPAPTTTKEPAPTTTKSAPTTPKEPAPT	A; Status: preliminary A; Molecule type: mRNA A; Residues: 326-489 <ar2> A; Cross-references: EMBL:</ar2>	030; NID:g791149; PID:g79115
lass 1 #status predicted <mat> 6%; Score 633; DB 2; Length 489; 2%; pred. No. 5.2e-20; 33; Mismatches 252; Indels 44; Gaps paptitkepapitykepapitikepapityksppyytksppp 1 1 1 1 1 1 1 1 1 1 </mat>	C;Genetics:, A;Gene: Ext26G A;Gene: Ext26G C;Superfamily: hydroxypro C;Keywords: glycoprotein; F;1-23/Domain: signal sec	e-rich glycoprotein broxyproline ce #status predicted <sig< td=""></sig<>
335 PKEPAPTTTKSAPTTPKEPAPTTTKEPAPTTTKEPAPTTTKSAPTTPKEPAP	Query Match Best Local Similarity Matches 149; Conservs	.6%; Score 633; DB 2; Length 489; .2%; Pred. No. 5.2e-20; e 33; Mismatches 252; Indels 44; Gap
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OM protein - protein search, using sw model
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Run on: April 26, 2002, 16:32:55; Search time 62.75 Seconds (without alignments) 795.232 Million cell updates/sec

Title: Perfect score: Sequence: AA7
7323
1 MAWKTLPIYLLLLSVFVIQ......ARAITTRSGQTLSKVWYNCP 1361

Scoring table:

Searched: 100059 seqs, 36664827 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

100059

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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PRINTS; PRO0438; GFCYSKNOT.
SMART; SM00214; VWC; 2.
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SMART; SM00216; VWD; 4.
SMART; SM00216; VWD; 4.
PROSITE; PS010022; EGF 1; UNKNOWN_1.
PROSITE; PS01185; CTCK_1; 1.
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InterPro; IPR000561; EGF-like.
InterPro; IPR002400; GF cysknot.
InterPro; IPR001007; VWFC.
InterPro; IPR001007; VWFC.
InterPro; IPR001846; Vwd.
Pfam; PF000007; Cys_knot; 1.
Pfam; PF000094; vwd; 4.
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EMBL; M74027; AAA59875.1; --
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Q06852;
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                       STRAIN-NCIB 10682;
MEDLINE-9320931; PubMed-8458832;
Fujino T., Beguin P., Aubert J.-P.;
Fujino T., Beguin P., Aubert J.-P.;
"Organization of a Clostridium thermocellum gene cluster cellulosomal scaffolding protein CipA and a protein possi in attachment of the cellulosome to the cell surface.";
J. Bacteriol. 175:1891-1899(1993).
-!- SUBUNIT: ASSEMBLED INTO MONO-LAYERED CRYSTALLINE ARRA-
-!- SUBCELLULAR LOCATION: CELL WALL.
-!- SIMILARITY: CONTAINS 4 S-LAYER HOMOLOGY (SLH) DOMAINS
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GLY/PRO/SER/THR-RICH.
SLH 1 (INCOMPLETE).
SLH 2.
SLH 3.
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POTENTIAL.

CELL SURFACE GLYCOPROTEIN

4 X 156 AA APPROXIMATE REF
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Pred. No. 7
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.9e-31;
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__YEAST
__ANYH_YEAST STANDARD; PRT; 1367 AA.
P08640; P08068;
01-AUG-1988 (Rel. 08, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
20-AUG-2001 (Rel. 31, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
GLUCCOAMYLASE S1/S2 PRECURSOR (EG 3.2.1.3) (GLUCAN :
GLUCCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCCHYDROLASE).
STA1 OR STA2 OR MAL5 OR YIRO19C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-S288C / AB972;
Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.
Barrell B.G., Badcock K., Edward S., Devlin K., F.
Chircher C. M., Connor R., Copsey T., Dear S., Devlin K., F.
Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K.,
Lyuis E., Lye G., Moule S., Moule T., Odell C., Pearson D.
Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.
Walsh S.V., Whitehead S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1601
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                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-242 AND 762-1331 FROM MEDLINE-87194600; Pubmed-3106330; Yamashita I., Nakamura M., Fukui S.; Yamashita I., Nakamura M., Fukui S.; Tene fusion is a possible mechanism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomycetales;
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
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                                                                                                                                                               MEDLINE-89031230; PubMed-3141213;
Pardo J.M., Tanez E., Zalacain M., Claros
"Similar short elements in the 5' regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                    STRAIN-SPX101-1C;
                                                                                                                                                                                                                                                                             SEQUENCE OF 1-31 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                  Bacteriol.
  m Saccharomyces cerevisiae.";
S. Lett. 239:179-184(1988).
CATALYTIC ACTIVITY: HYDROLLYSIS OF T
GLUCOSE RESIDUES SUCCESSIVELY FROM
WITH RELEASE OF BETA-D-GLUCOSE.
SIMILARITY: TO S.POMBE SPBC215.13.
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TO (
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                                                                                                                                         APTPSSSTTESSSAPVTSSTTESSSAPVPTPSSSTTESSSTPVTSSTTESSSAPVPTPSS
                                                                                                                                                                   TTTKSAPTTTKEPAP----TTTKSAPTTPKEPSPTTTKEPAP----TTPKEPAPT-TPKK
                                                                                                                                                                                                                                                                             PAPTTTKEPAPTTKSAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPTP--
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                                                                                                                                                                                                                                                                                                                                                                                                                   SSTTAPATPTTTSCTKEKPTPPTTTSCTKEKPTPPHHDTTPCTKKKTTTSK-TCT---KK
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 PTTPKEPAPTTPKETAPT-TPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDK
                              VPTPSSSTTESSSAPVPTPSSSTTESSSAPVT-
                                                     TPEKPAPTTPEELAPT-TPEEPTPTTPEEPAP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Multigene family.
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GLUCOANYLASE S1/S2.

SER/THR-RICH.

N-LINKED (GLONAC. . .) (POTEN N-LINKED (GLONAC. . .))
                                                                                                                                                                                                                                                      -SSTTESSSAPVTSSTTESSSAPVPTPSSSTTESSSA
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Pred. No. 7.
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MUCL_HUMAN STÄNDARD,

P15941; p15942; p13931; p17626; Q14128; carriage

Q1-JAN-1990 (Rel. 13, Created)

Q1-JAN-1990 (Rel. 14, Last sequence update)

Q1-APR-1990 (Rel. 14, Last sequence update)

20-AUG-2001 (Rel. 40, Last annotation update)

MUCIN 1 PRECURSOR (POLYMORPHIC EPITHELIAL MUCIN) (PEM) (PEMT)

(EPISIALIN) (TUMOR-ASSOCIATED MUCIN) (CAMA) (1823AG) (PEA-

CTMOR-ASSOCIATED EPITHELIAL MEMBRANE ANTIGEN) (EMA) (1823AG) (PEA-

CTMOR-ASSOCIATED EPITHELIAL MEMBRANE ANTIGEN)

(PUMOR-ASSOCIATED ANTIGE)
                                                SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-90202794; PubMed-2318825;
Ligtenberg M.J.L., Vos H.L., Gennissen
"Episialin, a carcinoma-associated muci
"Episialin, a carcinoma-associated muci
                                                                                                                                                                                                              TISSUE-Pancreas;

MEDLINE-90368716; PubMed-2394722;

Lan M.S., Batra S.K., Q1 W.-N., Metzgar R.S.,

"Cloning and sequencing of a human pancreatic
J. Biol. Chem. 265:15294-15299(1990).
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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Metazoa; Chordata; C
Metazoa; Primates; (
                            265:5573-5578(1990)
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Catarrhini; Hominidae;
                                                                         nissen A.M.C., Hilkens ed mucin, is generated variants with alternate
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hominidae;
                                                                                                                                                                                                                                                                 Hollingsworth
tumor mucin cI
                                                                               alternative
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Ъуа
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SEQUENCE:
TISSUE=Thyroid;
MEDLINE=96183746; PubMed=8608966;
MeDLINE=96183746. Reydar I., Wreschner D.H.;
Weiss M., Baruch A., Keydar I., Wreschner D.H.;
"Preoperative diagnosis of thyroid papillary carcinoma by transcriptase polymerase chain reaction of the MUC1 gene.'
Tht. J. Cancer 66:55-59(1996).
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SEQUENCE FROM N.A.
MEDLINE-91097524; PubMed-2268309;
Lancaster C.A., Peat N., Duhig T., Wilso
Taylor-Papadimitriou J., Gendler S.J.;
"Structure and expression of the human
"Structure and expression unit.";
"173:1019
  TISSUE-Lung;
MEDLINE-96181716;
Yu C.J., Yang P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coding for a breast-ca
Gene 93:313-318(1990).
[8]
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MEDLINE=91033045; PubMed=1688329;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           "A highly immunogenic expressed by carcinoma
J. Biol. Chem. 263:128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tsarfaty I., Hareuveni M., Horev J., 2 Jeltsch J.M., Garnler J.M., Lathe R., "Isolation and characterization of an coding for a breast-cancer-associated
                                                                                                                                                                                                                                             SEQUENCE OF 1-109
                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-90088473;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PARTIAL SEQUENCE FROM N.A. MEDLINE-88330762; PubMed-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eur. J. Biochem. 189:475-486(1990).
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MEDLINE=90276414; PubMed=2112460;
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J. Biol. Chem. 265:15286-15293(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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Biochem. 189:463-473(1990).
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263:12820-12823(1988).
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PubMed=2597151;
  PubMed=8604237; ., Shew J.Y., Ho
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MIM; 113720; -
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Submitted (OCT-1992) to
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SIGNAL 1 23 POTENTIAL.
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PIR; A35175; A35175.
PIR; B35175; B35175.
PIR; S10218; S10218.
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PTM: HIGHLY GLYCOSYLATED (N-AND O-LINKED
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  TTTAKDKTTERDLRTTPETT-----TAAPKMTKETATTTEKTTESKITATTTQVTSTT
                           APDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAP----
                                                                             DTRPAPGSTAPPAHGYTSAPDTRPAPGSTAPPAHGYTSAPDTRPAPGS-
                                                                                                    SDKPAP -- TTPK ---
                                                                                                                            TRPAPGSTAPPAHGYTSAPDTRPAPGSTAPPAHGYTSAPDTRPAPGSTAP-PAHGYTSAP
                                                                                                                                                     TPKEPAPTTPKG----TAPTTLKEPAPTTP----
                                                                                                                                                                              GSTAPPAHGVTSAPDTRPAPGSTAP-PAHGVTSAPDTRPAPGSTAPPAHGVTS---
                                                                                                                                                                                                                              PPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAP
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                                                     - IHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAATKPEM
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FLQIYKOGGFL -> VS
ISOFORM).
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MISSING (IN SECRI
T -> A (IN REF. 1)
P -> Q (IN REF. 2)
P -> Q (IN REF. 3)
A -> T (IN REF. 3)
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Pred. No. 3.2e-19;
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-DTRPAPGSTAPPAHGVTSAPDTRPA

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Q25460;
30-MAY-2000
30-MAY-2000
20-AUG-2001
                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor.send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002964; Adhesive_plaq.
InterPro; IPR002965; P_rich_extensn.
PRINTS; PR01216; ADHESTVEI.
PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PARTIAL SEQUENCE, MEDLINE-83135732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-91025829; PubMed-1367451;
Filpula D.R., Lee S.M., Link R.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mytilus edulis (Blue mussel).
Eukaryota; Metazoa; Mollusca; I
Mytiloidea; Mytilidae; Mytilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1038
                                                                                    EMBL; X54422; CAA38294.1;
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BIOL. Chem. 258:2911-2915(1983).

FUNCTION: PROVIDES ADHESIVENESS TO THE MUSSEL'S FOOT. MUSSELS PRODUCE ONE OF THE STRONGEST WATER INSOLUBLE GLUE. THE MUSSEL'S ADHESIVE IS A BUNDLE OF THREADS, CALLED A BYSUS, FORWED BY A FIRROUS COLLAGENOUS CORE COATED WITH ADHESIVE PROTEINS.

SUBCELLULAR LOCATION: SECRETED.

TISSUE SPECIFICITY: PRODUCED BY THE BYSSAL GLAND.

DOMAIN: ALMOST EXCLUSIVELY COMPOSED OF REPEATS OF A DECAPEPTIDE.

PTM. THE DECAPEPTIDE A.F.-P-Y-P-T-Y-K IS POST-TRANSLATIONALLY

MODIFIED AS FOLLOWING: THE SIXTH AND SEVENTH RESIDUES ARE

HYDROXYLATED AND THE PENULTIMATE IS A 3,4-DIHYDROXYPHENYLALANINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TQDTTP--FKITTLKTTTLAPKVTTTKKTITTT--EIMNKPEETAKPKDRATNSKATTPK
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Hydroxylation.
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JOO (Rel. 39, Last seguence update)
JOO (Rel. 40, Last annotation update)
PLAQUE MATRIX PROTEIN (POLYPHENOLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      functional repetition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AND POST-TRANSLATIONAL PubMed-6298211;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  3,4-dihydroxyphenylalanine-
decapeptide in the adhesive
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TYKSKSIYPSSYKPKKTYPPT---YKPKLTYPPTYK---
                       TLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQKPTKAPKK---P
                                                                   AKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTSTTTQDTTPFKIT
                                                                                                                                                           KAKPSYP----PTYKAKPSYPPTYKAKPTYPSTYKAKPSYPPTYKPKISYPPTYKAKPSY
                                                                                                                                                                            KPAPTTPKETAPTTPKEPA--PTTPKKPA-PTT----PETPPPTTSEVSTPTTTKE----
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                                                                                                        PPT-YKAKPSYPPTYKAKPTYKAKPTNPSTYKAKPSYPPTYKAKPSYPPTYKAKPSYPPT
                                                                                                                                 PTTIHKSPDESTPELSAEPTPKALENSPK----EPGVPTT--KTPA----ATKPEMTTT
                                                                                                                                                                                                                                          PAPTTPKEPAPTTPKGT---APTTLKEPA--PTTPKKPA--PKELAPTTTKG-PTSTTSD
                                                                                                                                                                                                                                                                                                                         KPT-----YPSTYKA----KPSYPASYKAKPSYPPTYKSKSSYPSSYKPKKTYPPTYK
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                                                                                                                                                                                                                                                                                                                                                                               PPTYKAKPTYKAKP-----TYPST-YKAKPSYP----PSYKAKPSYPPTYKAKPTYKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                   -PTYKAKPSYPPTYKAKPTYKAKPSYPPTYKAKPSYPPTYKAKPSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -VKTSYSAPYKPPTYQPLKKKVDYRPTKSYPPTYGSKTNY
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3; Mismatches
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Pred. No. 4.9e-16;
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 PKPSYPPSYKPKITYP
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RESULTATION OF THE PROPERTY OF
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RI GENOMICS 41:119-122(1997).

CC -!- FUNCTION: BINDS IN A SPECIES-SPECIFIC MANNER TO THE ZONA PELLUCIDA OF THE EGG. MAY BE INVOLVED IN GAMETE RECOGNITION AND/OR SIGNALING.

CC -!- SUBUNIT: PROBABLY FORMS COVALENT OLIGOMERS.

CC -!- SUBURIT: PROBABLY FORMS COVALENT OLIGOMERS.

CC -!- TISSUE SPECIFICITY: IN TESTIS; PERMARILY IN HAPLOID SPERMATIDS.

CC -!- TISSUE SPECIFICITY: IN TESTIS; PERMARILY IN HAPLOID SPERMATIDS.

CC -!- DOMAIN: THE MAM DOMAINS PROBABLY MEDIATE SPERM ADDRESION TO THE ZONA PELLUCIDA.

CC -I DOMAIN: THE MAM DOMAINS PROBABLY MEDIATE SPERM ADDRESION TO THE GENERATIOS.

CC -I DOMAIN: THE MAM NIGRATION THROUGH THE REPRODUCTIVE TRACTS, THE MUCIN-LIKE DOMAIN MIGRATION TO THE OVIDUCTAL ISTHMUS.

CC -I DOMAIN: THE VOYED DOMAINS 2 AND 3 MAY MEDIATE COVALENT OLICOMERIZATION (BY SIMILARITY ON HUMAN INTESTINAL MUCIN MUC2).

CC -I SIMILARITY: CONTAINS 3.5 MAM DOMAINS.
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IPR002919; TIL.

LICERPRO; IPR002919; TIL.

R InterPro; IPR001007; VWFC.

InterPro; IPR0011046; VWd.

Pfam; PF01826; TIL; 4.

Pfam; PF01826; TIL; 4.

Pfam; PF02345; TILa; 4.
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MEDLINE-97271566; PubMed-9126492;
Gao Z., Harumi T., Garbers D.L.;
"Chromosome localization of the m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome
[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glockner G., Scherer
Tsui L.C., Rosenthal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-2379
MEDLINE=99018118; F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human
Finkaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                        EMBL; AF053356; AAC78790.1; EMBL; U83191; AAC51208.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 2338-2700 FROM N.A.
                                                                                                                                                                                                                                                                                                                      MIM; 602372;
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                                                                                                                                                                                                                                                                                                                                                                                                                   send an
                                                                                                                                                                                                                                                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restrictly non-profit institutions as long as its content if idea and this statement is not removed. Usage by and its requires a license agreement (See http://www.isb-scend an email to license@isb-sib.ch).
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. 8:1060-1073(1998).
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); PubMed=9799793;
ierer S., Schattevoy l
thal A.;
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SMART; SM00216;
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                                                                                                                                                          SAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPT----PTTI
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                                                                                  EPSPTTTKEPAPTTPKEPAPTTPKKPA-----PTTPKEPAPTTPKEPAPTTTKKPAPTAP
                                                                                                           -PTTPTE-KPTIPTEKPTISTEKPTIPTEK-PTISPEKLTIPTEKLTIPT---EKPTIPT
                                                                                                                                                                                  TEKPTIPSE-KPTIPSEKPTISTEKPTVPTEE--PTTPTEETTTYMEEPVIPTEKPSIPT
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                 PTPTTPEEPAPTTPKAAAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPT
                                   EKPTISTEKPTIPTEKPTISPEKLTIPT-EKLTIPTEKPTIPIEETTISTEKL--TIPTE
                                                                        EKPTISTEE - - PTTPTEETTISTEKPSIPMEKPTLPTEETTTSVEETTISTEKLTIPM - -
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S; PR01217; PRICI
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SM00214;
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; VWC; 1.
; VWC_def;
; VWD; 3.
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%; Pred. No. 3.3e
64; Mismatches
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66 X HEPTAPEPTIDE REPEATS (
(MUCIN-LIKE DOMAIN).
VWED 1 (PARTIAL).
VWED 2.
VWED 3.
VWED 4.
VWED 4.
                                                                                                                                                                                                                                                                                                                                          MW;
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                                                      -PTTPEKPAPTTPEELAPTTPEE
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                                                 Query Match
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Matches 170
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Ol-JAN-1990 (Rel. 13, Created)
Ol-JAN-1990 (Rel. 13, Last sequence update)
Ol-MAR-1992 (Rel. 21, Last annotation update)
EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH
                                                                                                                                                                DOMAIN
SEQUENCE
                                                                                                                                                                                                        DOMAIN
REPEAT
REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Specific expression of a novel cell wall hydroxyproline-rich plycoprotein gene in lateral root initiation."; Genes Dev. 3:1639-1646(1989).
-I- FUNCTION: HAS A SPECIALIZED STRUCTURAL FUNCTION, POSSIBLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eu Asteridae; euasterids I; Solanales; Solanaceae; Nicot NCBI_TaxID=4097;
                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
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MEDLINE-90128263; Pub
Keller B., Lamb C.J.;
                                                                                                                                                                                                                                                                                                    REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                 Repeat;
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    292 AETTTK-GPALTTP--KEPTPTT---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX.

PTM: EXTENSINS CONTAIN A CHARACTERISTIC REPEAT OF THE PE
SER-PRO(4). THE PROLINE RESIDUE IS HYDROXYLATED AND THEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLYCOSYLATED.
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at; Cell wall;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THE MECHANICAL PENETRATION
                                                 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKET--A
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                                                                         Similarity
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                                        Score 551; DB
Pred. No. 1.5e
64; Mismatches
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H-A-P-P.
2 X 7 AA
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3 X APPROXIMATE TANDEM REPEATS.
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--PKEPASTTPKE---PTPTTIKSAPTTPKEPAP
                                                                                                                                                                                                                                                                                                                                                                                                          Signal;
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.5e-15;
les 304;
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8
                                                                    PTPKALENSPKEPGVPTTKTPAATKP
                                                                                            PPPRQIHSPPPPHWQPRTPTPTYGQPPSPPTFSAPPPRQIHSPPPPHRQPRPPTPTYGQP
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RESULT 8
               ACCOCC OCCOCC REPARE TO THE PROPERTY OF THE PR
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Mushynski W.;
"Sequence and structure c
neurofilament subunit.";
Gene 68:307-314(1988).
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P19246; 061959;
01-NOY-1990 (Rel. 16, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT
NEUROFILAMENT TRAVET HEAVY POLYPEPTIDE) (NF-H).
Shneidman P.S., Carden M.J., Lees J.F., Lazzarini R "The structure of the largest murine neurofilament revealed by cDNA and genomic sequences."; Brain Res. 464:217-231(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE-89121513; PubMed-3220257;
                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=89089138; PubMed=3145094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
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Rodentia;
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Sciurognathi;
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thi; Muridae;
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                                                                                                                 R.A.;
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Murinae; Mus
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                                                                          (NF-H)
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Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.

Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.

CC -!- FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M, CC AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER.

CC NF-H HAS AN IMPORTANT FUNCTION IN MATURE AXONS THAT IS NOT SUBSERVED BY THE TWO SMALLER NF PROTEINS.

CC -!- PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P, NFH IS COMESTION OF THE SERINES IN THIS MOTIF. IT IS COMESTION OF THE SERINES IN THE FORMATION OF THE SERINES IN THE FORMATION OF COMESTION OF ALLBER.

CC INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), THE COMMITTEN OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), THE COMMITTEN HELONGS TO THE INTERRED DEVELOPMENTALLY AND CONCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION.

CC -!- SIMILARITY: BELONGS TO THE INTERREDIATE FILAMENT FAMILY.

CC -!- SIMILARITY: BELONGS TO THE INTERREDIATE SHOWN IN POSITIONS 534

CC --- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN IN POSITIONS 534
Query Match
Best Local S
Matches 216
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SEQUENCE FROM I
STRAIN-SWISS WI
Carden M.J.;
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between
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD;
                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Intermediate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00038; filament; 1.
 Local Sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IL; M24496; AAA39813.1; IL; M2349; AAA39813.1; JL; M24494; AAA39813.1; JL; M24495; AAA39813.1; JL; M35131; AAA39809.1; AZ35131; CAA83229.1; JT0368; QFMSH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way if the street of the stree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGI:97309; Nfh.
                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS00226; IF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR001664; IF.
 Conservative
                                                                                                WEBSTER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 filament;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N.A.
                                                                                                AA;
                                                                                                                 7.3%;
27.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Brain;
                                                                                                116612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coiled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOINED.
JOINED.
JOINED.
ALT_FRAME.
                                                                                COIL 2B.

K -> QA (IN REF. 2 AND 3).
A -> AR (IN REF. 2 AND 3).
S -> T (IN REF. 2 AND 3).
L -> G (IN REF. 2 AND 3).
P -> PREAKSP (IN REF. 3).
MISSING (IN REF. 3).
G -> A (IN REF. 3).
V -> M (IN REF. 3).
V -> N (IN REF. 2 AND 3).
T -> N (IN REF. 2 AND 3).
T -> N (IN REF. 2 AND 3).
   81;
   Score 533; DB 1;
Pred. No. 1.2e-14;
1; Mismatches 330
                                                                                                                                                                                                                                                                                                    LINKER 1.
COIL 1B.
LINKER 12.
COIL 2A.
LINKER 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                   GLU-RICH (ACIDIC)
50 x 6 AA TANDEM
                                                                                                                                                                                                                                                                                                                                                                                                  GLU/LYS-RICH
COIL 1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neurone; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEATS
                                       Length 1087;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                         K-S-P-A-E-A
       158;
   Gaps
       38;
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RESULT 9
TONA_TRYCR
ID TONA_T
ID TONA_T
ID TONA_T
ID 101-NOV
DT 01-NOV
DT 20-AUG
DT 20-AUG
DT 20-AUG
DT ENALLD
GN TONA.
OS Trypan
OC Eukary
OX NCBI_T
RN [1]
RN [1]
RP SEDALN
RY MEDLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               망
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                                                                                                                                                                                                                                                                                                       ΔÃ
                                                                                                                                                                                                                                                                                                                                         밁
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                                                                                                                      01-NOV-1991 (Rel. 2
01-NOV-1991 (Rel. 2
20-AUG-2001 (Rel. 4
SIALIDASE (EC 3.2.1
                                                                                                                                                                                   TCNA_TRYCR P23253;
                                                                                                                                                                                                                                                                               1083
                                                                                                                                                                                                                                                                                                                                                                                                    1007
 SEQUENCE FROM N.A.
STRAIN=SILVIO X-10/4;
MEDLINE=91277609; PubMed=1711561;
                                                                           Eukaryota;
                                                                                        Trypanosoma_cruzi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                404
                                                             NCBI_TaxID=5693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TKSAPTTPKE-PSPTTTKEPA----PTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP-APTTTKEPAPTTPKEPAPTTTKEP----APTTTKSAPTTPKEPA----PTTPKKPA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TKSRVKEEAKSPGEAKSPGEAKSPA----EAKSPGEAKS-PGEAKSPGEAKSPAEPKSPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EECRIGEGPSPFSLTEGLPKIPSIST - - HIKVKSEEMIKVVE
                                                                                                                                                                                                                                                                               TKGEK 1087
                                                                                                                                                                                                                                                                                                            TTTEK 904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TLPTPKTEAKESKKDEAPKEAPKPKVEEKKETPTEKPKDSTAEAKKEEAGEKKKAVASEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPAAVKSPGEAKSPGEAKSPAEAKSPAEAKSPIEVKSPEKAKTPVKEGAKSPAEAKSPEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                 PKETAPTTPKEPAPTTPKKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RP--PEQVKSPAKEKAKSPE--KEEAKTSEKVAPKKEEVKSPVKEEVKAKEPPKKVEEEK
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                                                                                                                                                                                                                                                                                                                                                                      EPTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETA
                                                                                                                                                                                                                                                                                                                                         -PK-MEAKVKEDDKSLSKEP--SKPKTEKAEKSSSTDQKESQPPE-
                                                                           Euglenozoa;
                                                                                                                                                                                                     STANDARD;
                                                                                                                        20, Created)
20, Last sequence update)
40, Last annotation update)
.1.18) (NEURAMINIDASE) (NA)
                                                                             Kinetoplastida;
                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                       1162
                                                                                                                                                                                                                                                                                                                                                                                                      ----KDTKEEKTTESRKPEEK-----
                                                                              Trypanosomatidae;
                                                                                                                           (MAJOR
                                                                                                                             SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEPAPTTPKET
                                                                                                                                                                                                                                                                                                                                              ---KTTEDKA 1082
                                                                                Trypanosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -KSEKET
                                                                                                                             ANTIGEN)
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Best Local
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CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trop.
                                                                                                                                                                                                                                                                        REPEAT
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                       HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The Trypanosoma cruzi neuraminidase contains bacterial neuraminidases, YWTD repeats of the receptor, and type III modules of fibronectin.
                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     trypomastigotes."
Trop. Med. Parasi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-91376547; PubMed-1896773;
Prioli R.P., Mejia J.S., Aji T., Al
"Trypanosoma cruzi: localization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                     Phosphorylation
                                                                                                                                                                                                                                                                                                                                                   Hydrolase;
                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002860; Pfam; PF02012; BNR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pereira M.E.A., Mejia
                                                                                                                                                                                                                                                                                                             REPEAT
 712
                        414
                                                  652
                                                                         367
                                                                                                 599
                                                                                                                        308
                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Exp. Med. 174:179-191(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P. Med. Parasitol. 42:146-150(1991).

PUNCTION: DEVELOPMENTALLY REGULATED NEURAMINIDASE IMPLICATED IN PARASITE INVASION OF CELLS.

CATALYTIC ACTIVITY: HYDROLYSIS OF 2,3-, 2,6- AND 2,8-GLYCOSIDIC LINKAGES JOINING TERMINAL NON-REDUCING N- OR O-ACYLNEURAMINYL RESIDUES TO GALACTOSE, N-ACETYLHEXOSAMINE, OR N- OR O-ACYLATED NEURAMINYL RESIDUES IN OLIGOSACCHARIDES, GLYCOPROTEINS, GLYCOLIPIDS OR COLOMINIC ACID.

SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPT-ANCHOR SUBCELLULAR LOCATION: ATTACHED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO FAMILY 33 OF SIMILARITY: CONTAINS 3 BNR REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEVELOPMENTAL STAGE: MAXIMAL ACTIVITY IN TRYPOMASTIGOTES, MINIMUM IN EPIMASTIGOTES AND NO DETECTABLE IN AMASTIGOTES.
MISCELLANEOUS: THE VARIABLE LENGTHS OF THE LONG TANDEM REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN COULD ACCOUNT IN PART FOR
                                                                                                                                                                                                                                                                                                                                                                                     JH0557; JH0557.
                                              TPSTPADSSAHSTPSTPVDS----SAHSTPSTPADSSAHGTPSTPVDSSAHGT----
                                                                                                                       TPTTPKE-PASTTPKEPTPTTIKSAPTTPKEPAPTTTKSAPTTPKEPAPTTTKEPAPTTP
                       KEPTP-TTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAPTTPKEPAPTTTKEPS
 VDSSAHGTPSTPADSSAHSTPSTPADSS-----
                                                                                                                                                                                                                                                                                                                                                                                                              M61732; AAA30255.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R.P.;
                                                                                                                                                                                                                                                                                                                                                 Glycosidase; Glycoprotein; Repeat;
                                                                                                                                                 Conservative
                                                                                                                                                                                                                                    163
209
458
589
342
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34
174
220
588
1120
342
394
1125
                                                                                                                                                            7.28; 29.48;
                                                                                                                                                                                                                                                                                                                                                                           BNR.
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                                                                                                                                                                         100;
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                                                                                                                                                            Score
Pred.
                                                                                                                                               Mismatches
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                                                                                                                                                           530.5;
No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLYCOSYL HYDROLASES
AHSTPSTPADSSAHSTPSTPVDSSA
                                                                                                                                                            ; DB 1;
.6e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pereira M.E.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequences similar to
low density lipoprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matzilevich
                                                                                                                                                                                                                                                                                                                                                   GPI-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                               Indels
                                                                                                                                                                       Length
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                                                                                                                                                                        1162;
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                                                                                               -PSTP
                                                                                                                                               Gaps
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                                                                      413
                       472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CANTON-S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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PPOC. NATI. ACAD. SCI. U.S.A. 90:1536-1540(1993).
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-I FUNCTION: MIGHT FUNCTION AS A CALCIUM-SEQUESTERING "SPO-
-I CA+2 PER MOL OF PROTEIN.
-I SUBUBNIT: HOMODIMER (PROBABLE).
-I SUBCELLULAR LOCATION: CYTOPLASMIC; HYPODENSE COMPARTMEN-
-I TISSUE SPECIFICITY: SOMA AND AXONS OF PHOTORECEPTOR CEI
-I TISSUE SPECIFICITY: SOMA AND AXONS OF PHOTORECEPTOR CEI
-I COMPOUND EYES AND OCELLI.
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Pred. No. 1.3e-14;
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-> E (IN REF. 2).
2110417E0B0E7CFE
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-> V (IN REF. 2).

-> T (IN REF. 2).

-> E (IN REF. 2).

-> T (IN REF. 2).
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> T (IN REF.
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2).
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                                                                                                                                                                                                                                                             ---PAPTTPKKPAPKE
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DOMAIN SEQUENCE

184 213 872

192 221 101677

MW.

NONAPEPTIDE 2. w; 98CC70D7C75FF3C4

DOMAIN DOMAIN DOMAIN

Signal; CHAIN

Repeat;

Hydroxylation

21 21 124

20 872 41 872

POTENTIAL.
ADHESIVE PLAQUE MATRIX PROTEIN.
NONREPETIVE LINKER.
TANDEM REPEATS OF Y-K-[PS]-K-[IPP-[PST]-[ST].
NONAPEPTIDE 1.

Y-K-[PS]-K-[IP]-[ST]-Y-

PRINTS;

PR01217; PRICHEXTENSN

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RESULT 11
FP1_MYTCO
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Q25434;
30-MAY-2000
                                                                                                                                                                                                                                                 InterPro; IPR002964; Adhesive_plaq.
InterPro; IPR002965; P_rich_extensn
PRINTS; PR01216; ADHESIVEI.
                                                                                                                                                               use by non-profit institutions as long modified and this statement is not remove entitles requires a license agreement (so or send an email to license@isb-sib.ch).
                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                Mytiloidea; Mytilidae;
NCBI_TaxID=42192;
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                                                                                                                                            EMBL;
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20-AUG-2001
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                                                                                                                                           D63777; BAA09850.1;
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(Rel.)
(Rel.
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39, Last sequence update)
40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                             Y., Takeyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sea mussel).
Mollusca; B
lae; Mytilus.
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                                                                                                                                                                                     is not removed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              872
                                                                                                                                                                        (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                            There are no restrictions on ng as its content is in no
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85 YPTKRYQPTYGSKTNYPPIYKPIAKKLSSYKAIKTTYPAYKAKTSYPPSYK-----HKIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T-YKPKISYPPTYKPKASYVSSYKSKKTYPPTYKPKISYPPTYKPKPSYPPTYKPKITYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YPPTYK-----PKITYP--PTYKQKPSYPPSYKPKTTYPPTYK-----PKITYPPTYK
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                              MPRVRKPKTT--PTPRKMTSTMPELNPTSRIAEAMLQTTTRPNQ
                                                                                                                                                                                                                                                                                                                                                                                                                           TT--PKGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKPAPT-TPKGTAPTTPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          K-PKPSYPPTYKPKITYPPT-YKPKPSYPTPYKQKPSYPPIYKSKSSYPTSYKSKKTYPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPT----TTKEPAPTTTKSAPTTPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYPSIYKPKASYVSSYKSKKTYPPTYKPKISYPPTYKPKPSYP----PTYKPKVTYPPTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAPTTPKEPAPTT----PKEPTPTT--PKEPAPTTKEPAPTTPKEPAPT-APKKPAPTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RKPSYTPYKPKATYPPTYKPKITYP----PTYKRKPSYT-----PYKPKTTYPPTYKPKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAPT-TPKEPAPT--TTKEPAPTTPKEPAPTTTKEPAPTTTKSAPTTPKEPAPTT--PKK
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YPPTYKPKISYPPTYKPKITYPPTYKPKISYPPAYKPKISYPSQ
                                                                                          VTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQ---KPTKAPKKP-TSTKKPK-T
                                                                                                                            ISYPSTYKAKP-----SYPPTYKPKPSYASSYKPKIRYPPTYKPKPSYASSYK-----PK
                                                                                                                                                           RTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTSTTTQDTTPFKITTLKTTTLAPK
                                                                                                                                                                                                                          IHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKT----TERDL
                                                                                                                                                                                                                                                            PPTYKPKITYPPTYK-PKPSYPPSYRPKITYPPTYKPKKSYPQAYKSKGSYPPSYQPKKT
                                                                                                                                                                                                                                                                                             PTT--PKETAPTTPKEPAPTTPK--KPAPTTPET-----PPPTTSEVSTPTTTKEPTT
                                                                                                                                                                                                                                                                                                                             -----PKITYPPTYK-PKPSYPTPYKQKPSYPPIYKSKSSYPTAYKSKKTY
                                                                                                                                                                                                                                                                                                                                                          EPAPTTPKEPAPTTPKGTAPTTLKEPAPTTP----KKPAPKELAPTTTKGPTSTTSDKPA
                                                                                                                                                                                                                                                                                                                                                                                                PTYKPKITYPPTYK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -PTTPEEPAPTTPKAAAPNTPK-EPAPTTPKEPAPTTP----KEPAPTT--PKETAP
                                                                                                                                                                                             -PPSYKPKKTYPPTYK----PKISYPPTYK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                               -RYPPTYKPKP----SYASSYKPKIRYPPTYKPKPSYASSYKPKIT
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29.28;
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Pred. No. 3.7
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3.7e-14;
                                                                                                                                                                                             -TKPSYPASYKRKTSYPPTYKPK
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RESULT 12

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01-0CT-1994
01-0CT-1994
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                                                                                                                                              REPEAT
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          REPEAT
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                                                                                                                                                                                                                                                                Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- ALTERNATIVE PRODUCTS: A NUMBER OF DIFFERENT MAY BE PRODUCED BY ALTERNATIVE SPLICING.
-i- TISSUE SPECIFICITY: SKIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "P-domains as shuffled cysteine-rich modules in integumentary
"P-domains as shuffled cysteine-rich modules in integumentary
C.1 (FIM-C.1) from Xenopus laevis. Polydispersity and genetic
polymorphism.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
INTEGUMENTARY MUCIN C.1 (FIM-C.1) (FRAGMENT).
Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                     Pfam; PF00088; trefoil;
                                                                                                                                                                                                                                                                                                                                 EMBL; L02115; AAA74725.1; -. PIR; A45155; A45155.
                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- PTM: EXTENSIVELY O-GLYCOSYLATED.
-i- SIMILARITY: CONTAINS 6 P-TYPE (TREFOIL) DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFECTIONS. PROTECTS THE EPITHELIA FROM -!- SUBCELLULAR LOCATION: SECRETED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                               SMART;
                                                                                                                                                                                                                                                                                                                         HSSP; P04002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUC1_XENLA
                                      DOMAIN
                                                                             REPEAT
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                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                InterPro; IPR000519; P_trefoil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93077556; PubMed=1447205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TROUBLEST. 7: 267:24620-24624(1992).

BE INVOLVED IN DEFENSE AGAINST MICROBIAL FUNCTION: COULD BE INVOLVED IN DEFENSE AGAINST MICROBIAL FUNCTION:
                                                                                                                                                                                                                                                                                             SM00018; P;
                                                                                                                                                                                                                                                                         Amphibian skin; Glycoprotein; Alternative splicing
                                                                                                                                                                                                                                                                                    PS00025;
                                     402
412
420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus.
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                                                                                                                                                                                                                                                                                    P_TREFOIL;
                                     THR-RICH.
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3-2.
3-3.
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P-TYPE
8 X APF
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                                     2-8.
2-9 TYPE 2.
P-TYPE 3.
12 X APPROXIMATE TANDEM REPEATS,
                                                                                                                                                                                                                                              ALA/THR-RICH.
                                                                                                                                                                                                                                                       X 8 AA APPROXIMATE TANDEM REPEATS
                                                                                                                                              APPROXIMATE
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                                                         KEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKPAPTT
                                                                                                                                                                               KKPAPTTPKEPAPTTPKEPAPTTTKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEKLA
                                                                                                                                                                                                                                          PSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKEPAPTTPKEPAPTTP
                                                                                                                                                                                                                                                                       VKPSKREMCGSKGITKKQ----CKKKNCCFDPKGHGGIHCFHRKPKGHSHEEHTTTTK-
                                                                                                                                                                                                                                                                                                     --PTTKEPAPT---TPKEPAPTAPKKPAPTTPK---
                                                                                                                                                                                                                                                                                                                               GKAPATAAAPVPTTAASKAPTTAAAATHSTAAAAAPTTAASAAKSKERSTSSSSEEEHCH
                                                                                                                                                                                                                                                                                                                                                  EPAPTTTKEPAPTTTKS-APTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPA-
                                                                                                                                                                                                                                                                                                                                                                                                                      TPTTPKEPASTTPKEPTPTTIKSAPTTPKEPAPTTTKSAPTTPKEPAPTTTKEPAPTTPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTAAAVAATGKDTTAAAEGSAAAEKTAA-----AGEVSAPPT--AAVAATGEDATT----
                                                                                                                    PTTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPTTPKAAAPNTPKEPAPTTPKEPAPTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -TAPTT----PKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELA
                                                                                                                                                                                                                                                                                                                                                                                           AAATAAAETTAAAGEAPTTTAPATTAAGKAPTTAAATAPTTAAAGAPTTAT
                                                                                                                                                                                                              -APTTIQIATTTT---TPTTT---
                               -TTTTTKATTTTTTSGECKMEPSK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                   TTTTKATPTTT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67774 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48;
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3-5.
3-6.
3-7.
3-9.
3-10.
3-11.
3-12.
p-TYPE 4.
p-TYPE 5.
p-TYPE 5.
BY SIMILARITY.
BY SIMIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 509.5; DB 1;
Pred. No. 6.6e-14;
48; Mismatches 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F085277F1ED2FD40 CRC64;
                                                                                                                                                   -TTTKATTTTT----TPTT----
                                                                                                                                                                                                              TTTTKATPTT-----
                                                                                                                                                                                                                                                                                                   EPAPTTPKEPAPTTTKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          662;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247;
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                                                                                                                     650
                                                                                                                                                                               590
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RESULT 13
RPB1_HUMAN
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         use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                           between
the Euro
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE=95347616; PubMed=7622068;

Mita K., Tsuji H., Morimyo M., Takahashi E., Nenoi M.,

Ichimura S., Yamauchi M., Hongo E., Hayashi A.;

"The human gene encoding the largest subunit of RNA polymerase II.";

Gene 159:285-286(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-92178992; PubMed-1542581;
Wintzerith M., Acker J., Vicaire S., Vigneron M
"Complete sequence of the human RNA polymerase
Nucleic Acids Res. 20:910-910(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-1992
20-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P24928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RPB1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE-92178992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLR2A
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                                                                                                                                                                                    SUBUNÍT: RNA POLYMERASE II CONSISTS OF 12 DIFFERENT SUBUNITS.
SUBCELLULAR LOCATION: NUCLEAR.
PTM: THE TANDEM 7 RESIDUES REPEATS CAN BE HIGHLY PHOSPHORYLATED.
THE PHOSPHORYLATION ACTIVATES POL2.
MISCELLANEOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES AR
FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA
                                                                                                                                                                                                                                                                                                 FUNCTION: DNA-DEPÉNDENT RNA POLYMERASE CATALYZES THE TRANSCI
OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES
SUBSTRATES.
CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPH
                                                                                                                                         III FOR 5S AND TRNA GENES.
SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY
                                                                           European
                                                                                                                                                                       PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND
                                                                                                                                                                                                                                                                                    RNA(N)
                                                                         SWISS-PROT entry is copyright. It is produced the swiss Institute of Bioinformatics and to buropean Bioinformatics Institute. There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTSTTTODTTPFKITTLKTTTLAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPQVADCKVAPSSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQKPTKAPKKPTSTKKPK----T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNA POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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21,
40,
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 II LARGEST SUBUNIT
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polymerase II largest subunit.";
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                                                              as
                             http://www.isb-sib.ch/announce/
                                            Usage
                                                              its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EC
                                                                                          and the
                                                                                                          through a collaboration
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                                             У
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                                                                         restrictions
                                                                                                                                                                                                                                                                                                     PYROPHOSPHATE
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                                               and
                                                                                             EMBL
                                                                                                                                                                          POLYMERASE
                                                                                                                                                                                                                                                                                                                                                   TRANSCRIPTION
                                               for
                                                                                             outstation
                                               in no way
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RESULT 14
RPB1_MOUSE
ID RPB1_M
AC P08775
DT 01-NOV
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N MIM; 1800501; --

R Interpro; IPR000684; RNA_pollA.

R Interpro; IPR00722; RNA_pol_A.

DR Interpro; IPR002879; RNA_pol_A2.

Pfam; PF00623; RNA_pol_A2.

DR Pfam; PF01854; RNA_pol_A2: 1.

DR Pfam; PF01854; RNA_pol_A2: 43.

DR Pfam; PF01854; A3.

DR Pfam; PF01854; RNA_pol_A2: 43.

DR Pfam; PF01854; RNA_pol_A2: 43.

DR Pfam; PF01854; RNA_pol_A2: 43.

DR Pfam; PF01854; A3.

DR Pfam; PF0
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Best Local :
RPB1_MOUSE
P08775;
01-NOV-1988
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BL; X74874; CAN52862.1;
BL; X74873; CAN52862.1;
BL; X74872; CAN52862.1;
BL; X74871; CAN52862.1;
BL; X74871; CAN52862.1;
BL; X74871; CAN52862.1;
BL; X74870; CAN52862.1;
BL; X74870; CAN52862.1;
R; S21054; S21054.
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31; Conservative
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(Rel. 09, Created
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1; Mismatches
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Pred. No. 2.
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2.8e-13;
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CONFLICT
CONFLICT
SEQUENCE
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                                                  Pfam; PF00623; RNA_POL_A; 1.

Pfam; PF01824; RNA_POL_A2; 1.

PROSITE; PS00115; RNA_POL_II_REPEAT; 42.

Transferase; DNA-directed RNA polymerase; Transcription; Zinc; Repeat;

Transferase; DNA-directed RNA polymerase; Transcription; Zinc-finger.

DNA-binding; Nuclear protein; Phosphorylation; Zinc-finger.

C2H2-TYPE (POTENTIAL).

ZN FING 71 87 C2H2-TYPE (POTENTIAL).
                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Proc. Natl. Acad. Sci. U.S.A. 82:7934-7938(1985).
                                                                                                                                                                       InterPro: IPR000684; RNA_polII_repeat InterPro; IPR000722; RNA_pol_A. InterPro; IPR002879; RNA_pol_A2.
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MEDLINE=92178992; PubMed=1542581;
Mintzerith M., Acker J., Vicaire S., Vigneron M., Kedinger C.;
"Complete sequence of the human RNA polymerase II largest subunit.";
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MEDLINE-86068017; PubMed-2999785;
Corden J.L., Cadena D.L., Ahearn J.M. Jr.,
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Mammalia; Eutheria; Rodentia;
MCBI_TaxID=10090;
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20-AUG-2001 (Rel. 40, Last annotation update)
DNA-DIRECTED RNA POLYMERASE II LARGEST SUBU
POLR2A OR RPO2-1 OR RPII215.
                                                                                                                                                                                                                               MGD; MGI:98086;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: RNA POLYMERASE II CONSISTS OF 12 SUBCELLULAR LOCATION: NUCLEAR. PTM: THE TANDEM 7 RESIDUES REPEATS CAN BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THE PHOSPHORYLATION ACTIVATES POL2.
MISCELLANEOUS: THREE DISTINCT ECONTAINING RNA POLYMERASES FOUND IN BUKARVOTIC NUCLET: POLYMERASE I FOR THE RIBOSOWAL RNA PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBSTRATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      III FOR 5S AND TRNA GENES. SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leic Acids Res. 20:910-910(1992).
FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE
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M14101; AAA40071.1;
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AA; 217175
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CARBOXYL-TERMINAL 7-RESIDUE
P -> R (IN REF. 1 AND 2).
MISSING (IN REF. 1 AND 2).
MW; 7D76F38FD92A657E CRC64;
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Sciurognathi; Muridae;
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largest subunit
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Query Match
Best Local Similarity
Matches 180; Conserv

Conservative

101;

Mismatches

168;

Indels Length

95;

Gaps

47;

6.8%;

Score 498.5; DB 1 Pred. No. 4.3e-13;

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P16884; Q63368;
O1-AUG-1990 (Rel
O1-FEB-1994 (Rel
                                                                                                    Dautigny A Jolles P.;
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01-FEB-1994 (Rel. 28,
20-AUG-2001 (Rel. 40,
NEUROFILAMENT TRIPLET
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Breen K.C., Robinson P.A., Wion D., Anderton B.H.;
Partial sequence of the rat heavy neurofilament polypeptide
Identification of putative phosphorylation sites.";
FEBS Lett. 241:213-218(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                           MEDLINE=88309090; PubMo
Dautigny A., Pham-Dinh
                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEFH OR NFH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NEUROFILAMENT HEAVY POLYPEPTIDE)
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                                                                         large neurofilament subunit (NF-H) of the rat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SY-SPTSPSY-SPTSPSY-SPTSPNY-SPTSPNYT-PTSP-SYSPTSP-SYSPTSPNY-T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rat).
a; Chordata;
                                                                                                                           PubMed=2457365;
Dinh D., Rousse
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                            154:1099-1106(1988)
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                                                                                                                              Felix J.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-89 AND 243-313
MEDLINE-87080760; PubMed-2878
Robinson P.A., Wion D., Ander
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00038; filament;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Intermediate
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L; X13804; CAA32038.1; F
L; M21964; AAA41695.1; L; J04517; AAA41692.1; A30796; A30796; A30796; A325649; B25649; B25649; B25649; B25649; S02003; S02000; S020000; S020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTIONING OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), THE LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND COINCLDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION.

SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
CAUTION: REF. 1 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBSERVED BY THE TWO SMALLER NF PROTEINS.

PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEDTIDE K-S-P, NFH PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF. IT IS THOUGHT THAT PHOSPHORYLATION OF NFH RESULTS IN THE FORMATION OF INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OF AXONAL CALIBER.

PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M. P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NATI. ACAD. SCI. U.S.A. 86:2463-2467(1989)
FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE
AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF
NF-H HAS AN IMPORTANT FUNCTION IN MATURE AXONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ONWARD AND IS LONGER DUE TO A FRAMESHIFT.
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OM protein - protein search, using sw model

April 26, 2002, 16:26:07; Search time 61.21 Seconds (without alignments) 500.359 Million cell updates/sec Run on:

AA7 7323 1 MAWKTLPIYLLLLLSVEVIQ.....ARAITTRSGQTLSKVWYNCP 1361 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 212252 seqs, 22503292 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No. Score Match Length DB ID 1 5.22 7.1 805 4 US-09-103-429A-4 Sequence 4, Appli 3 US-08-36-36-36 Sequence 5, Appli 3 US-08-30-26-36-36 Sequence 5, Appli 4 498.5 6.8 1721 3 US-08-708-51-5 Sequence 5, Appli 5 G.8 1721 3 US-08-708-51-5 Sequence 5, Appli 6 G.8 1721 3 US-08-708-51-5 Sequence 5, Appli 6 G.8 1721 3 US-08-708-51-5 Sequence 5, Appli 8 488.5 6.7 826 5 EVT-US9-00018-2 Sequence 2, Appli 10 426.5 6.2 960 4 US-09-219-849-5 Sequence 2, Appli 11 428.5 6.2 960 4 US-09-219-849-5 Sequence 2, Appli 11 424.5 5.8 1867 2 US-08-479-537A-5 Sequence 5, Appli 12 424.5 5.8 1867 2 US-08-479-537A-5 Sequence 2, Appli 12 424.5 5.8 2035 2 US-08-479-537A-5 Sequence 2, Appli 12 424.5 5.8 2035 2 US-08-479-537A-5 Sequence 2, Appli 12 424.5 5.8 2035 2 US-08-479-537A-5 Sequence 2, Appli 12 424.5 5.8 2035 2 US-08-479-537A-5 Sequence 2, Appli 12 424.5 5.8 2035 2 US-08-479-537A-5 Sequence 2, Appli 12 424.5 5.8 2035 2 US-08-479-537A-5 Sequence 2, Appli 12 424.5 5.8 2035 2 US-08-479-537A-5 Sequence 2, Appli 12 424.5 5.8 2035 2 US-08-479-537A-5 Sequence 2, Appli 12 424.5 5.8 2035 2 US-08-479-537A-5 Sequence 2, Appli 21 US-08-477-5098-103 Sequence 2, Appli 21 US-08-477-5098-103 Sequence 2, Appli 21 US-08-477-5098-103 Sequence 103, Appli 21 US-08-477-5098-103 Sequence 103, Appli 21 US-08-477-5098-103 Sequence 103, Appli 24 417 5.7 837 1 US-08-477-5098-103 Sequence 103, Appli 24 417 5.7 837 1 US-08-477-5098-103 Sequence 103, Appli 24 417 5.7 837 1 US-08-477-5098-103 Sequence 103, Appli 24 417 5.7 837 1 US-08-477-5098-103 Sequence 50, Appli 24 417 5.7 837 1 US-08-477-5098-103 Sequence 103, Appli 24 417 5.7 837 1 US-08-477-5098-103 Sequence 50, Appli 24 417 5.7 837 1 US-08-477-5098-103 Sequence 50, Appli 24 417 5.7 837 1 US-08-48-68-53 Sequence 50, Appli 24 417 5.7 837 1 US-08-477-5098-103 Sequence 50, Appli 24 417 5.7 837 1 US-08-477-5098-103 Sequence 50, Appli 24 417 5.7 837 1 US-08-477-5098-103 Sequence 50, Appli 25 417 5.7 837 1 US-08-477-5098-103 Sequence 50, Appli 25 417 5.7 837 1 US-08-477-5098-103 Sequence 50, Appli 25 4 417 5.7 837			ф			SUMMARIES	
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7.1%; Score 522; DB 4; Length 805; 27.8%; Pred. No. 3e-25;

Query Match Best Local Similarity

Sequence 65, Appl Sequence 126, Appl Sequence 126, Appl Sequence 4, Appl1 Sequence 2, Appl1 Sequence 6, Appl1 Sequence 6, Appl1 Sequence 28, Appl Sequence 26, Appl Sequence 26, Appl	Sequence 6, Appli Sequence 84, Appl Sequence 114, App Sequence 26, Appl
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ALIGNMENTS

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Sequence 4, Application US/09103429A

Sequence 4, Application US/09103429A

Patent No. 6187558

GENERAL INFORMATION:

APPLICANT: Granados, Robert R

APPLICANT: Granados, Robert R

TITLE OF INVENTION: DNA and Related Products and Methods

TITLE OF INVENTION: ADDRESS:

CORRESPONDENCES:

ADDRESSEE: Brown, Pinnisi & Michaels, P.C.

STREET: 118 No. 6187558th Tioqa

CTITY: Ithaca

STATE: NY

COUNTY: USA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
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THEIR FUNCTIONAL MOTANTS, VARIANTS, ANALOGS AND FRAGMENTS
FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
SPECIES INFECTIONS
   40;
                                                                                                         :: || | | RDCAPGTEFKFSAQTCVHAALAGCTLPGPPAETT---QAPATTQ--APTTT 119
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                            TSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTIKSAP-----TTP 335
                                                                                        -TKSAPTTPKEPAPTTTKEPAPTTPKEPAPTTTKEPAPTTTK 383
                                                                                                                                               SAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPTPTTPKEPAPTTKEPAPTTPKEPAPTA 443
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                                                   TALGLVAARPEVSDAEKNPALHEPHPDXP--PAEQXXLLPXEYDCTKFYYCEYGLKFIAP 66
    Gaps
                                                                                                                                                               PKKPAPTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAP
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   342;
   Indels
 211;
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APPLICANT: PETETSEN, CATOLYN
TITLE OF INVENTION: PEPTIDES,
TITLE OF INVENTION: THEIR FUNCTIONAL MUTANI'S
TITLE OF INVENTION: FOR TREATMENT AND DETECT
TITLE OF INVENTION: SPECIES INFECTIONS
NUMBER OF SEQUENCES: 30
CORRESPONDENCES: 30
CORRESPONDENCE ADDRESS:
STREET: 385 Sherman Avenue, Solite 6
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             836 ELSAEPTPKALENSPKEPGVPTTKTPAATKPE 867
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 33;
 Conservative
                                                                                      KEPAPTT----
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226;
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174 SITSGELKDPNKQATISGSRSCGWKQGYSIDSSTGFRVDSITGLPTDPYPNCPFNPVTGN 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----TTTKSAPTTTK 492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        406 КЕРАРІТРКЕРІРІТРКЕРАРІТКЕРАРІТРКЕРАРІАРККРАРІТРКЕРАРІТРКЕРАР
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1837;
                                                                                                             PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
7.0%; Score 510.5; DB 3;
Best Local Similarity 20.8%; Pred. No. 4.1e-24;
Matches 314; Conservative 109; Mismatches 530;
                                                                                                                                                                                                                                                                                                                      NAME: Veruy, man...
REGIGTRATION NUMBER: 30,518
                                                                                                  APPLICATION NUMBER: US 60/026,062 FILING DATE: 13-SEP-1996 ATTORNEY/AGENT INFORMATION: NAME: Verny, Hana
                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -------
                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
TELEFAX: 650-324-1678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1837 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTKEPSPTT-----
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MOLECULE TYPE: protein
US-08-928-3618-5
                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
94306-1840
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52;

RESULT 3 5202236-25 ;Patent No. 5202236 ; APPLICANT: MAUGH, KATHY J.;ANDERSON, DAVID M.;STRAUSBERG,

207 PKITTAKPINPRPSLPPNSDTSKETSLTVNKETTVETKETTTNKQTSTDGKEKTTSAKE 266 267 TQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKE----PASTTPKE 322 380 ITTKSAPTIPKEPAPTIPKKPAPT-TPKEPAPTT----PKEPIPTIPKEPAPTTKEP--- 431 379 480 11 : || : || : |: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: || :|: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: || 533 322 585 SYPPTYKAKPSYPPTYKAKPSYPPTYKAKPSYPPTYKAKPTYKAKPTYPS 382 635 КЕРАРТТРКЕРАРТТ----РКЕРАРТТРКЕТАРТТ--РКСТАРТТКЕРАРТТРККРАРК 688 Indels 175; Gaps 54 ------YPPTYK--AKPS------YPPTYKPKKTYPPTYKPKPP 92 634 ELAPITIKEPISTISDKPAPIIPKGTAPIIPKEPAPIIPKEPAPIIPKGTAPIILKEPA- 747 802 849 601 661 895 323 PTPTTIKSAPT-TPKEPAPTTTKSAPTTPKEPAPTTTKEPAPTTPKEPAPTTTKEPA--P 432 -APTTPKEPA--PTAPKKPA--PTTPKEPA--PTTPKEPA--PTTTKEPS--PTTPKEPA -PTTTKSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKEPA--PTTPKEPA----PTTPKKP A--PITPKEPA--PITPKEPA--PITTKKPA--PIAPKEPAPITPKETAPTTPKKLIPTT 586 PEKLAPTTPE--KPAPTTPEELAPTTPEEPT--PTTPEEPA-PTTPKA--AAPNT----P -PTTPKKPAPKELAPTTTKGPT--STTSDKPAPTTPKETAPTTPKEPAPTTPKKPA--PT ---TPETPPPTTSEVSTPTTTKE----PTTIHKSPD-----ESTPELSAEPT-PKALENS YKAKPSYPPTYKAKPSYPPTYKAKPSYPPTYKAKPSYPPTYKAKPTYKAKPTYPSSTYKAK PKEPGVPTTKTPAA-----TKPEMTTTAKDKTTERDLRTTPETTTAAP-----KMT Length 744; N L.; MCCANDLISS, RUSS; WEI, TENA; FILPULA, DAVID TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE 6.9%; Score 506.5; DB 6; 29.9%; Pred. No. 2.6e-24; Live 78; Mismatches 308; CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-MAY-1990
APPLICATION NUMBER: 82,456
FILING DATE: 07-AUG-1987
APPLICATION NUMBER: 933,945
FILING DATE: 24-NOV-1986
APPLICATION NUMBER: 560
FILING DATE: 13-SEP-1984 Conservative Best Local Similarity Matches 239; Conserv ; LENGTH: 744 5202236-25 ; SEQ ID NO:25 Query Match 481 534 323 689 748 547 ; PROTEIN 803 850 662 SUSAN ð å d à g ŏ g ð g a à ò qq Ω g à ΩD ò g δ g δ g ò

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                                                                                                                                   Sequence 3, Application US/09103429A
Sequence 3, Application US/09103429A
Patent No. 6187558
GENERAL INFORMATION:
APPLICANT: Granados, Robert R
APPLICANT: Wang, Ping
TITLE OF INVENTION: A No. 6187558el Invertebrate Intestinal Mucin
TITLE OF INVENTION: CDNA and Related Products and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 29.1%; Pred. No. 8.8e-24;
Matches 200; Conservative 25; Mismatches 207; Indels 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,429A
FILING DATE: 24-JUN-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Brown, Pinnisi & Michaels, P.C. STREET: 118 No. 6187558th Tioga CITY: Ithaca STATE: NY COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
ATTORNEY/AGRATION:
NAME: Michaels, Christopher A
REGIGSTRATION NUMBER: 34,390
REFERENCE/DOCKET NUMBER: BII-39
TELEPHONE: (607) 256-2000
TELEPHONE: (607) 256-3628
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 786 amino acids
TYPE: amino acid
STRANDEDNESS: single
TYPE: amino acid
STRANDEDNESS: single
TYPE: Innear
MOLECULE TYPE: POTCLEIN
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRGANISM: Trichoplusia ni
; TISSUE TYPE: peritrophic membrane
US-09-103-429A-3
                        : | ::| | :|
720 YKAKPTYPSTYKAKPTYPST 739
896 KETATTTEKTTESKITATTT 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
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US-09-103-429A-3
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Qy do	478EPAPTIT
oy o	362 CGAGTHFSFELQQCDHIELVGGTLPGGESEEVDVDEDA-CTGWYCFTEF1EWEF1EWG-F *20 518 APTTPKEP537
QQ	421 ADFSIDHLLPHESDCGQYLQCVHGQTIARPCPGNLHFSPATQSCESPVTAGCQVFECDSD 480
QY Dp	538PKEPAPTTPKEPAPTTKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTP 594
QY	595 EKPAPITPEELAPITPEEPAPITPKAAAPNIPKEPAPITPKEPAPITPKE 652
q	
g d	
Qy	
QΩ	633 TAAPIT-AAPAPNTIVTVPPTAAPTAAPPTVAHAPNTTAAPVTTTS 677
Qy	3 DK
Q Q	3
RESULT US-08- US	SULT 5 GU-700-651-5 Sequence 5, Application US/08700651B Patent No. 6015882 Sequence 5, Application US/08700651B Patent No. 6015882 APPLICANT: ILECANT: LEECH. APPLICANT: LEECH. APPLICANT: LECANT: LECAND. TITLE OF INVENTION: YOR PROPHILAXIS AND TREATMENT OF CYPTOSPORTING, DNAS AND RNAS TITLE OF INVENTION: POR PROPHILAXIS AND TREATMENT OF CYPTOSPORTING DATE: 1997-08-14 TITLE OF INVENTION: WHEER: US/08/700,651B CURRENT FILING DATE: 1997-08-14 CURRENT FILING DATE: 1995-04-03 NUMBER OF SEQ ID NOS: 15 SEQ ID NO 5 LENGTH: 1721 TYPE: PRET ORGANISM: CYPTOSPORIGIUM PAIVUM S-08-08-08-08-08-08-08-08-08-08-08-08-08-
Que Bes Mat	Query Match 6.8%; Score 496.5; DB 3; Length 1721; Best Local Similarity 22.1%; Pred. No. 2.9e-23; Matches 295; Conservative 86; Mismatches 495; Indels 459; Gaps 43;
Qy	110 PTSPPSSKRAPPPSGASQTIKSTIKRSPKPPNKKKTKKVIESEEITEVKDNKKNRTKKKP 169
qq	82 PTDPYSNCPFNPVTG-NLVSRSTGKTIPNTYAGGYYRSNETK 121
Oy.	170 TPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRPSLPPNSDTSK 229
a :	TDGKEKTTS

 Db 115: Qy 107! Db 120:	3 NSINKDPVINTQYSNTTGNIINPETGKVIPGSLPGSLNYPSFNTPQQTDEITGK 9MLSDETNICNGK 7 PVDTYTGLPYDPGYGIIDPATKLPIPGSVAGDEITGFVNTFNFDVPGYGIIDPATKLPIPGSVAGDEITGFVNTFNFDVPGYGIIDPATKLPIPGSVAGDEITGFVNTFNFDVPGYGIIDPATKLPIPGSVAGDEITGFVNTFNFDFVPGYGIIDPATKLPATKLPIPGSVAGDEITGFVNTFNFDFVPGYGIIDPATKLPATKLPATKLPATKLPATKLPATKLPATKLPATKL
 Oy 11. Db 12.	
RESULT 6 US-08-928-1 Sequence Sequence TITLE TIT	6 Application US/089283611 No. 6071518 AL INFORMATION: PETETIONS, P. CAL INFORMATION: PETETIONS, P. CAL OF INVENTION: PETTIONS, P. CAL OF INVENTION: PETTIONS, P. CAL OF INVENTION: PETTIONS, P. CAL OF INVENTION: PETTIONS PETTIONS, P. CAL OF INVENTION: PETTIONS PETTIONS PETTIONS PETTIONS PETTIONS PETTIONS PETTIONS PETTION: PETTION PETTION: PETTION PETTION: PETTION NUMBER: US/08/928, LING DATE: 13-SEP-1997 ASSIPICATION NUMBER: US 60/026, LING DATE: 13-SEP-1997 ASSIPICATION NUMBER: US 60/026, LING DATE: 13-SEP-1997 ASSIPICATION NUMBER: 30,518 FERRENCE/DOCKET NUMBER: 30,518 FERRENCE/DOCKE
Query M Best Lo Matches	' Match Local Similarity 22.1%; Pred. No. 2.96-23; Les 295; Conservative 86; Mismatches 495; Indels 459; Gaps 43;
	PTSPPSSKKAPPPSGASQTIKSTIKRSPKPPNKKKTKKVIESEBITEVKDNKKNRTKKP 169
Oy 170 Db 122 Qy 230 Db 168	TERPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRPSLPPNSDTSK 229 I

		QY 1079MDYLPRVPNQGIIINP
δy	275 AKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAPTT 334	Db 1207 PVDTVTGLPYDPSTGEIIDPATKLPIPGSVAGDEILTF
Dp	209	Qy 1107 -PVDGLTTLRNGTLV 1120
VO 4	335 PKEPAPTITKSAPTIPKEPAPTITKEPAPTIPKEPAPTITKEPAPTITKSAPTIPKEPAP 394	
a ko	3395 TTPKKPAPTTPKEPAPTTPKEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKE 454	RESULT 7 US-07-638-431-2
Dp	310 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	; Sequence 2, Application US/07638431 ; Patent No. 51995355
Oy Pr	455 PAPTTPKEPAPTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPKE 508	GENERAL INFORMATION: APPLICANT: Hoffman, Stephen L. APPLICANT: Charoenvit, Yupin APPLICANT: APPLICANT:
g À	530 illililililililililililililililililili	n, Archard 1, Srisin FV; William O.
: A	116 PDEWCWLEKNGECEAKGATYVGVIGKDGRIENGMAFTMIPNDDTHVRFRFKVKDVGNTIS 475	⋛⋛
O. d.	514APTIPKEPPTTPKKP 533 1	, NUMBER OF SEQUENCES: 2 ; CORRESPONDENCE ADDRESSE: ; ADDRESSEE: A. David Spevack conterm: NAMPOR Building 1 T-12 National 1
3 8	534 ADWINDKEPAPITPKEPAPITIKKPAPIAPKEPAPITPKETAP 575	SIREET: Name Contact ; STREET: Dethords
ξ ć	AFITTAL APIOPSELFNEVYCDTCTAKYGAI	STATE: DELICEDED STATE: MD COUNTRY: USA
ò	576 TTPKKLTPTTPEKLAPTTPEKPAPTTPEBLAPTTPEEPTTPEEPAPTTPKAAAPNTPK 635	ZIP: 20814-5044 COMPUTER READABLE FORM:
e d	S90 GSPSKPTTTTTKATTTTTTLNPIITTTQKPTTTTTTKVPGKPP 634	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible
Qγ	APTTPKETAPTTPKGTAPTTKEPAPTTPKKPAPKELA	OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.24
QQ		CURRENT APPLICATION DAIA: ; APPLICATION NUMBER: US/07/638,431
δλ	692 PITIKEPISITSDKPAPTIPKG-TAPTIPKEPAPTIPKEPAPTIP 735	; FLILING DATE: 1991ULLU ; CLASSIFICATION: 424 ; ATTORNEY/AGENT INFORMATION:
qq	EDSNDEPTPGSQAGQTADISNDFFVQIRNSIGHF LET	NAME: Spevack, Avrom D. TELECOMMUNICATION INFORMATION:
ço ç	736 KGTAPTILKEPAPTIPKKPAPKELAPTITKGPTSTISSKPAPTIFKETAPTIFKAETA 722 736 KGTAPTILKEPAPTIPKKPAPKELAPTITKGPTSTISSKPAPTIFKETAPTIFKAETA 722 750 MYGT DEDDKGGNI VHPYTNOTMSGILSSVSYLAAKNITVDTDETYGLPIDTLIGYPLDPV 807	TELEPHONE: (301) 295-6759; TELEPRA: (301) 295-6759; TELEPRA: (301) 295-4033
8 8	793 PTTPKKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKS829	INFORMATION FOR SEC. S. SECURED SEC. SECURED S
: a		7.5
Qy	830	; MOLECULE TYPE: protein us-07-638-431-2
qq	FSPEIEDGGIIPPEVAAANADKFKLSIPPSVP	6.7%;
کو ج	861 PAATKPEMTTTAKDKTTERDERTTPETTTAAFKMIKKIATITE 303 1	Best Local Similarity 26.4%; Pred. No. 3.5 Matches 153; Conservative 54; Mismatches
δλ		324
qq		273
δy ξ	961 TAKPKDRAINSKATTPKPQKPTKAPKKPTSTKKPKTWP998 	Qy 377 PAPITIKSAPITYKEF-APITEKKY AFILENGE AL DE CONTROL DE 333 PINPINPINPINPINPINPINPINPINPINPINPINPIN
70	RVRKPKTTPTPRKMTS-	Oy 433 PTTPKEPAPTAPKKPAPTTPKEPAPTTPKEPAPTT
QQ	1093 PIDGNNQLVNPETNSTVSGSTSGTTKPKPGIPVNGGGVVPDEEAKDQADKGKDGLIVPPT 1152	
۲۵۷ مرح	1023 SRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVEWPEVTPD 1078 : : :	Oy 491 TKEPAPITIKSAPITENENSPITINEEARIIENEN
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DB 1; Length 826; 9e-23; s 223; Indels 149; Gaps 34; -PTTPKKP-APTTPKEPAPTTPKE 548 TTKEPSPTTPKEPAPTTTKSAPTT 490 DETNICNGK------ 1106 orozoite surface protein Naval

PTTPKE : PSNPNE RAAAPN : SNPN		PC/TUS9200018 Stephen L. it, Yupin N. Richard N. Ailiam O. Protective malaria sporozoite surface protein immunogen and gene encoding immunogen and gene en	6.7%; Score 488.5; DB 5; Length 826; 26.4%; Pred. No. 3.9e-23; ive 54; Mismatches 223; Indels 149; Gaps 34;
Qy 549 PAPTTKKPAPTAPKEP-APTTFKI Db 493 PSNPNEPSNPNEPSNPNE Qy 608 TTPEEPTPTTPEEPAPTTPKAAAPP Qy 67 STANNEPLNPNEPSNP Qy 667 KGTAPTTLKEPAPTTPKKPAPKELA Db 565 SNPEEPNPEEP Qy 727 PKEPAPTTPKGTAPTTLKEPAPTTLK		92-00018-2 ence 2, Application pe ence 2, Application pe ence 2, Application pe ERAL INFORMATION: PPLICANT: Hoffman, St PPLICANT: Hoffman, St PPLICANT: Hoffman, St PPLICANT: Hoffman, St PPLICANT: ROGERS IV, ITLE OF INVENTION: IN ITLE OF INVENTION: PI ITLE OF INVENTION: PI ITLE OF INVENTION: PI ITLE OF INVENTION: PI STREET: MARDC Buildi STREET: MAGICAL Cent CITY: Betheada STARET: MOBLESSEE: A DAVIA STREET: MOBLESSEE: POWN STREET: MOBLESSEE: POWN COUNTRY: USA ITLE OF INVENTION DAVIA MEDIUM TYPE: FIOPPY COMPUTER: EADABLE FORM: MADIUM TYPE: POPCHON PELCANTING SYSTEM: PC SOFTWARE: PAPLICATION UNDER: ILECOMMUNICATION INFORMAT NAME: Spewack, AVTAM ILECOMMUNICATION INFORMAT TYPE: AMINO ACID TOPPOLOGY: linear ILECOMMUNICATION TYPE: PLOTEIN TYPE:	Query Match 6.7%; Sc Best Local Similarity 26.4%; Pr Matches 153; Conservative 54;

45; 377 PAPTTTKSAPTTPKEP-APTTPKKP-APTTPKEP-APTTPKEP-TPTTPKEPAPTTKEPA 432 490 549 PAPTITKKPAPTAPKEP-APTIPKETAPTIPKKLTPTIPEKLAPTIPEKPAPTIPEELAP 607 TIPEEPIPITPEEPAPITPKAAAPNIPKEP-APIIPKEPAPTIPKEPAPIIPKETAPTIP 666 564 667 КGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTT 726 727 PKEPAPTIPKGTAPTILKEPAPTIPKKPAPKELAPTITKGPISTISDKPAPTIPKETAPT 786 787 TPKEP-----APTTPKKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAE 840 650 LPIIPQKGNNIPSNLPENPSDSEVEYPRPNDNGENSNNTMKSKKNI---PNEPIPSPGDN 706 207 PKITTAKPINPRPSLPPNSDTSKETSLIVNKETTVETKETTTNKOTSTDGKEKTTSAKE 266 267 TOSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKE----PASTTPKE 322 -----YPPTYK--AKPS-----YPPTYKPKTYPPTYKPKLTYPPTYKPKP 79 PTTPKEPAPTAPK--KPAPTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTKSAPTT 491 TKEPAPTITKSAPTTPKEPSPTTTKEPAPTTPKEPA-PTTPKKP-APTTPKEPAPTTPKE PS------NPNEPSNPNEPSNPNE--PSNPKK-------PSNPNE--P 607 PKEPI------NPEESNPKEP----INPEDNENPLIQDEPIEPRNDSNVIPI 11 PKMTYPPTYKPKPSYPP------KPKIT----Indels 169; Length 652; ; Patent No. 5202236

**APPLICANT: MAUGH, KATHY J.; ANDERSON, DAVID M.; STRAUSBERG, SUSAN L.; MCCANDLISS, RUSS; WEI, TENA; FILPULA, DAVID

**ITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE Query Match 6.5%: Score 476.5; DB 6; Best Local Similarity 29.7%; Pred. No. 1.7e-22; Matches 221; Conservative 71; Mismatches 284; | | | | : | : | 307 PYKGHEERIPKPHRSNDDYVYDNNVNKNNKDEPEIPNNE 745 841 PTPKALENSPK-------EPGVPTTK 859 NUMBER OF SEQUENCES: 39
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-MAY-1990
APPLICATION NUMBER: 82,456
FILING DATE: 07-AUG-1987
APPLICATION NUMBER: 933,945
FILING DATE: 24-NOV-1986
APPLICATION NUMBER: 650,128
FILING DATE: 13-SEP-1984 ; LENGTH: 652 5202236-13 ;SEQ ID NO:13: 433 493 809 565 5202236-13 41 ; PROTEIN 엄 à g ŏ 셤 δ qq à q δ g ò g δ g δ g ò qq g ð q ò

324 TPTTIKSAPTTPKEPA-PTTTKSAPTTPKEPA-PTTTKEP----APTTPKEP-APTTKE 376

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755 AP-----KELAPTITKGPTST--TSDKPAPTIPKETAPTIPKEPAPTTPKKPAPTTP-- 804
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                                                                                                                        PTSPPSSKKAPPPSGASQTIKSTTKRSPKPPNKKKTKKVIESEEITEVKDNKKNRTKKKP 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -PTAPK-KPAPTTP---KEPAPTTPKEPA-PTTTKEPSPTTPKEPAPTTTKSAPTTTKEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          805 --ETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALEN----SPKEPGVPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      229 KETSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKVLAKP
                                                                                                                                                                                                                                                                                                            289 TPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTTTTKSAPTTPKEPAPTTKSAPT
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                                                                                                                                                                                                                                                                              -----RDPGPP----GAP
                                                                                                                                                                                                                    ----ppgapgpagpgs---
                                                                                          Indels 251;
                                                               Length 960;
                                                               Ouery Match 6.2%; Score 455.5; DB 4;
Best Local Similarity 23.0%; Pred. No. 5.5e-21;
Matches 195; Conservative 64; Mismatches 338;
                                                                                                                                                        23 PAGPPGSRD-PGPPGAPGPAGPPGSRDPGPPG------
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; OTHER INFORMATION: amino acid sequence US-09-219-849-5
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US-09-041-886-23
Sequence 23, Application US/09041886
; Patent No. 6235872
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GENERAL INFORMATION:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       170 TPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRPSLPPNSDTSK 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   290 PKAETTTKGPALITPKEPTPTTP--KEPASTTPKEPTPTTKSAPTTPKEPAPTTTKSAP 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146 DSSSGLSQGPA--RPYHPPPLFPPSPQPPDSTPRQPEASF------EPHPSVTPTGY 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -EPAPTTPKKPAPTTPKEPAPTTPKEPTPTTPKEPAPTTKEPAP-----TTPKEPAPTA- 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
5.8%; Score 428; DB 4; Length 1185;
Best Local Similarity 22.1%; Pred. No. 3.7e-19;
Matches 237; Conservative 114; Mismatches 429; Indels 292;
                                                 Peptides, Dependence and Methods of Use
APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependen
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
STATE: California
COUNTY: United States
ZIP: 92122
                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                                                                                                  ATTONNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-8949
INFORMATION FOR SED ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 1185 amino acids
                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-041-886-23
                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
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553 TTKKPAPTAPKEPAPTTPKETAPTTPKKLT-----PTTPE--KLAPTTPEKPAPTTPEEL 605 630 APN----TPKEPAPTTPKEP-----APTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAP 679 386 SQGPQGAPYPFPPVPTVTTSSATLSTVIATVASSPAGIKTASPPGPPPGKRAPSPGAYK 645 972 KATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQ 1031 417 SL----SVSNOP----PKYTOPSLPSQAVWSQGPPPPPPYGRLLANSNAHPGPFPPSTG 467 468 AOSTAHPPVSTHHHHHQQQQQQQQQQQQQHHGNSGPPPGAFPHPLEGGSSHHAHPYAM 527 680 TTPKKPAPKELAP---TTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPK 736 737 GTAPTILKEPAPTIPKKPAPKELAPTITKGPISTTSDKPAPTTPKETAPTTPKEPAPTTP 796 646 TATPPGYKPGSP----PSFRTGTPPGYRG----TSPPAGPGTFKPGSPTV--GPGPLPP 694 797 KKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDE--STPELSAEPTPKALENS--PKE 852 853 PGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKT-TESKIT 911 912 ATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTBIMNKPEBTAKPKDRATNS 971 ----TPEEPAP-----TTPKAA 821 EREREKERELERSVKLAQEGRAP----VECPSLGPVPHR-----PPFEPGSAVA----GENERAL INFORMATION:
APPLICANT: CHAMBON, Pierre
APPLICANT: ATATHE, RICH-Paule
APPLICANT: LATHE, RICH-Paule
APPLICANT: LATHE, RICH-Paule
APPLICANT: HARBUVENI, Mara
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR THE
TITLE OF INVENTION: TREATMENT OR PREVENTION OF A MALIGNANT TUMOR
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: P.O. BOX 1404 1032 TTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLP 1083 866 -TVPPYLGPDTPALRT--LSEYA------RPHVMSPGNRNHPFYVP 902 STATE: VICTIONIA
COUNTRY: United States
CONFORT: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,537A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PROOR APPLICATION DATA:
APPLICATION NUMBER: FR 90/13101
FILING DATE: 23-OCT-1990 ; Sequence 5, Application US/08479537A
; Patent No. 5861381 806 AR-----606 APTTPEEPTPT--US-08-479-537A-5 g δ g ò g ò q ò q à q ò g ò q ò q ò g

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1040 -PNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLSD 1098
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GENERAL INCORMATION:
APPLICANT: CHAMBON, Pierre
APPLICANT: KIENY, Marie-Paule
APPLICANT: LATHY, Marie
APPLICANT: HARBUVENI, Mara
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR THE
TITLE OF INVENTION: TREATMENT OR PREVENTION OF A MALIGNANT TUMOR
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ETNICNGKPVDGLTT-LRNGTLVAFRGHYFWMLSPFSPPSPARRITEVWGIPSPID 1153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -TKPEMTTTAKDK - - - TTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       728 KEPAPTIPKG----TAPTILKEPAPTIP-----KKPAPKELAPITIKGPISITSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAPDXRPXPGSTAPXAHGVTS----PPDXRPXPGSTAPXAHGVTSAPDXRPX----PGST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       531 TAPXAHGVTSAPDXRPXPGSTAP-XAHGVTSAPDXRPXPGSTAPXAHGVTS----APDXR
                                                                                                                                                                                            TKEPSPTTPKEPAPTT--TKSAPTTTKEPAPTT----TKSAPTTPKEPSPTTTK----E
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241 APDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS
                                                                                                                                                                                                                                                  301 APDXRP-XPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVT
                                                                              PKE--PAPTTKEP-----APTTPKEPAPTAPK----KPAPTTPKEPAPTT
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US-09-083-116-5
; Sequence 5, Application US/09083116
; Patent No. 6203795
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128 to 1737 constitute a repeated region wherein the repeat
20 amino acids, 17 of which are fixed. The number of such
repeats varies from 1 to 40."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            = CCT, CCC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Amino acid 134 is X1 = Xaa
which is the codon for Pro or Ala wherein Pro = CCT, CCC,
or CCG; and Ala = GCT, GCC, GCA, or GCG."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  333 ITPKEPAPTIT-----KSAPTIPKEP------APTITKEPAPTIPKEPAPTI 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             231 TSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKD-LAPTSKVLAKPT 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -TPTTPKEPASTTPKEPTPTTIKSAP 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Amino acid 147 is X2 = Xaa
which is the codon for Pro or Ala wherein Pro
or CCG; and Ala = GCT, GCC, GCA, or GCG."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Amino acid 144 is Y = Xaa
which is the codon for Thr or Asn wherein Thr
or ACG; and Asn = AAT or AAC."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 -- DNKPAPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1867;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Amino acids 1 to 21 are a 21 amino acid precursor sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.8%; Score 424.5; DB 2;
23.7%; Pred. No. 1e-18;
:ive 69; Mismatches 511;
                                                                                                                                                                                                                                                                                                         NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REPERBENCHOOLSONGER NUMBER: 017753-025
TELECHONE: (703) 836-6620
TELEPAX: (703) 836-620
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1867 amino acids
                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR91/00835
FILING DATE: 23-0CT-1991
PRIOR APPLICATION DATA:
                                                                                                                                           APPLICATION NUMBER: US 08/039,320
FILING DATE: 04-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/403,576
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          290 P-KAETTTKGP--ALTTPKEP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Peptide
LOCATION: 128.1727
OTHER INFORMATION: //
OTHER INFORMATION: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Peptide
LOCATION: 1..21
OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
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NAME/KEY: Peptide
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OTHER INFORMATION:
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Best Local Similarity
Matches 255; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY:
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                                                                                                  231 TSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKD-LAPTSKVLAKPT 289
                                                                                                                                                                         290 P-KAETTTKGP--ALTTPKEP------TPTTPKEPASTTPKEPTPTIKSAP 332
                                                                                                                                                                                                          PGSGSSTTQGQDVTLAPATEPASGSAATWGQDVTSVPVTRPALGSTTPPAHDVT---SAP 122
                                                                                                                                                                                                                                                        ---APTTTKEPAPTTPKEPAPTT 373
                                                                                                                                                                                                                                                                                 123 -- DNKPAPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS 180
                                                                                                                                                                                                                                                                                                                     374 TKE--PAPTTT-----KSAPTTPKEPAPTTPK----KPAPTTPKEPAPTTPKEPTPTT 420
                                                                                                                                                                                                                                                                                                                                              241 APDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               680 TTP-----KKPAPKELAPTTTKEPTSTTSDKPAP--TTPKGTAPTTPKEPAPTTP 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      728 KEPAPITPKG----TAPTILKEPAPITP-----KKPAPKELAPITIKGPISTISD 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    864 -TKPEMITIAKDK---TTERDLRITPETTTAAPKMIKETATTTEKITESKITATTTQVTS 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                         644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRAINSKATTPKPQ 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      821 APDXRPXPG----STAPXAHGVT----SAPDXRPXPGSTAPXAHGVTSAPDXRPXP- 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APXAHGVTSAPDXRPXPGSTAPXAH-----GVTSAPDXRPXPGSTA----PXAHG 957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      468 TKEPSPTTPKEPAPTT--TKSAPTTTKEPAPTT----TKSAPTTPKEPSPTTTK----B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             360 SAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    569 TPKETAP----TTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          625 IPKA----AAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGT-APTTLKEPAP
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                                                                                                                                                                                                                                                                                                                                                                                               421 PKE--PAPTTKEP-----APTTPKEPAPTAPK----KPAPTTPKEPAPTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     420 SAPDXRPXPGSTAPXAHGVTS----APDXRPXPGSTAPXAHGVTSAPDXRPX----PGST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          818 TITKEPTT-----IHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -GSTAPXAHGVTSAPDXRP--XPGSTAPXAHGVTSA-PDXRPX-------PGST
                                                                       Indels 241;
                                  Length 1867;
                              5.8%; Score 424.5; DB 4;
23.7%; Pred. No. 1e-18;
tive 69; Mismatches 511;
                                                                                                                                                                                                                                                333 TTPKEPAPTTT-----KSAPTTPKEP-----
                                              Similarity 23.7555; Conservative
                              Query Match
Best Local Simi
Matches 255;
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128 to 1727 constitute a repeated region wherein the repeat
20 amino acids, 17 of which are fixed. The number of such
repeats varies from 1 to 40."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Amino acid 134 is XI = Xaa
which is the codon for Pro or Ala wherein Pro = CCT, CCC,
or CCG; and Ala = GCT, GCC, GCA, or GCG."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Amino acid 144 is Y = Xaa
which is the codon for Thr or Asn wherein Thr = ACT, ACC,
or ACG; and Asn = AAT or AAC."
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which is the codon for Pro or Ala wherein Pro = CCT,
or CCG; and Ala = GCT, GCC, GCA, or GCG."
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SSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P. P. P. P. D. Box 1404
Alexandria
                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR91/00835
FILING DATE: 23-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,320
FILING DATE: 04-APR-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TORNEYANDER TORKIN TODIN L.
NAME: TESKIN NUMBER: 35,030
REGISTRATION NUMBER: 017753-025
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/403,576
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                       US/09/083,116
                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 0177
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 836-2021
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1867 amino acids
                                                                       United States
                                                                                                                                                                                                CURRENT APPLICATION DATA
                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 12B..1727
OTHER INFORMATION: //
OTHER INFORMATION: 12
OTHER INFORMATION: 26
OTHER INFORMATION: re
                                                                                                                                                                                                                     APPLICATION NUMBER:
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LOCATION: 144
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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CTHER INFORMATION:
CTHER INFORMATION:
US-09-083-116-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Peptide
LOCATION: 128..17:
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OTHER INFORMATION:
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OTHER INFORMATION:
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FEATURE:
NAME/KEY: Peptide
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STRANDEDNESS: sir
                                                       Virginia
                                                                     COUNTRY: United ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                              FILING DATE:
 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
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/note= "Amino acid 144 is Y = Xaa
which is the codon for Thr or Asn wherein Thr = ACT, ACC,
or ACG; and Asn = AAT or AAC."
                                                                                                                                                       /note= "Amino acid 147 is X2 = Xaa
which is the codon for Pro or Ala wherein Pro = CCT, CCC,
or CCG; and Ala = GCT, GCC, GCA, or GCG."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    625 TPKA----AAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGT-APTTLKEPAP 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 PGSGSSTTQGQDVTLAPATEPASGSAATWGQDVTSVPVTRPALGSTTPPAHDVT---SAP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTPKEPAPTTT-----KSAPTTPKEP-----APTTTKEPAPTTPKEPAPTT 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             374 TKE--PAPITI-----KSAPIIPKEPAPITPK----KPAPIIPKEPAPITPKEPTPII 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PKE--PAPTIKEP-----APTIPKEPAPTAPK----KPAPTIPKEPAPTIT 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 APDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   569 TPKETAP----TTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPT 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAPDXRPXPGSTAPXAHGVTS----APDXRPXPGSTAPXAHGVTSAPDXRPX----PGST 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231 TSLTVNKETTVETKETTTTNKQISTDGKEKTTSAKETQSIEKTSAKD-LAPTSKVLAKPT 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            472 APXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRP-XPGSTAPXAHGVTSAPDXRPXPGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       728 KEPAPTTPKG----TAPTTLKEPAPTTP------KKPAPKELAPTTTKGPTSTTSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 APDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---TPTTPKEPASTTPKEPTPTIKSAP
                                                                                                                                                                                                                                                                                                                                                                                                                                      241;
                                                                                                                                                                                                                                                                                                                                                                                            Length 2035;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                     /note- "Amino acids 1 to 21 are a 21 amino acid precursor sequence."
                                                                                                                                                                                                                                                                                                                                                                                            5.8%; Score 424.5; DB 2; 23.7%; Pred. No. 1.1e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative 69; Mismatches 511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             774 KPAP--TIPK----ETAPIIPKEPAPTIP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 290 P-KAETTTKGP--ALTTPKEP-----
                                                                                                                                                                                                                              FEATURE:
NAME/KEY: Peptide
LOCATION: 1..21
OTHER INFORMATION:
OTHER INFORMATION:
                   LOCATION: 144
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                  FEATURE:
NAME/KEY: Peptide
LOCATION: 147
OTHER INFORMATION:
OTHER INFORMATION:
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 255; Conserv
                                                                                                                                                                                                                                                                                                                                       US-08-479-537A-2
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such
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128 to 1899 constitute a repeated region wherein the
20 amino acids, 17 of which are fixed. The number of
repeats varies from 1 to 40."
                              1099 ETNICNGKPVDGLTT-LRNGTLVAFRGHYFWMLSPFSPPSPARRITEVWGIPSPID 1153
                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: PHARACEUTICAL COMPOSITION FOR THE TITLE OF INVENTION: PHARACEUTICAL COMPOSITION OF A MALIGNANT NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESSE: BURNS, DOANE, SWECKER & MATHIS, L.L.P. STREET: P.O. Box 1404
CITY: Alexandia STATE: Virginia STATE: Virginia STATE: Virginia STATE: Virginia
COUWTRY: United States
ZIP: 222313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,537A FILING DATE: US-JUN-1995 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 90/13101
FILING DATE: 23-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR91/00835
FILING DATE: 23-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 017753-025
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 23-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,320
FILING DATE: 04-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/403,576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release *1
                                                                                                                                                     Sequence 2, Application US/08479537A Patent No. 5861381 GENERAL INFORMATION:
APPLICANT: CHAMBON, Pierre
                                                                                                                                                                                                                                         KIENY, Marie-Paule
LATHE, Richard
HAREUVENI, Mara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
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LOCATION: 128.1899
OTHER INFORMATION: /r
OTHER INFORMATION: 20
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OTHER INFORMATION:
OTHER INFORMATION:
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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                                                                                                                                                                                          KPTKAPKKPTSTKFKFMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPNQT 1039
                                                                                                                                                                                                                                                                   1040 -PNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLSD 1098
                                      -TKPEMITTAKDK---TTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTS 919
                                                                       763 DXRFXPGSTAPXAHGVTSAPDXRPXPGST--APXAHGVTSAPDXRPXPGSTAPXAHGVTS 820
703 DXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAP 762
                                                                                                              920 TITQDITPFKITILKITILAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATIPKPQ 979
                                                                                                                                                 821 APDXRPXPG-----STAPXAHGVT-----SAPDXRPXPGSTAPXAHGVTSAPDXRPXP- 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09083116
| Patent No. 6203795
| GENERAL INPORMATION: APPLICANT: CHAMBON, Pierre
| APPLICANT: ATHE, KIChard
| APPLICANT: HARBUVENI, Warie Paule
| APPLICANT: HARBUVENI, Warie Paule
| APPLICANT: HARBUVENI, Warie Paule
| TITLE OF INVENTION: PHEMACEUTICAL COMPOSITION FOR THE
| TITLE OF INVENTION: PREATMENT OR PREVENTION OF A MALIGNANT TUMOR OF SEQUENCES: 5
| CORRESPONDENCE ADDRESS: 5
| CORRESPONDENCE ADDRESS: 5
| ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
                                                                                                                                                                                                                                                                                                                                             1099 ETNICNGKPVDGLTT-LRNGTLVAFRGHYFWMLSPFSPPSPARRITEVWGIPSPID 1153
                                                                                                                                                                                                                                                                                                                                                                            958 VTSAPDXRPXPGSTAPXAHGVTSA------PDXRPXPGSTAPXAHGVTSAPD 1003
                                                                                                                                                                                                                        869 -GSTAPXAHGVTSAPDXRP--XPGSTAPXAHGVTSA-PDXRPX--------PGST
                                                                                                                                                                                                                                                                                                      912 APXAHGVISAPDXRPXPGSTAPXAH------GVISAPDXRPXPGSTA----PXAHG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: WO PCT/FR91/00835
FILING DATE: 23-0CT-1991
APPLICATION NUMBER: US 08/039,320
FILING DATE: 04-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/403,576
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALLIDE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/083,116
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APPLICATION NUMBER: 08/479,537
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REGISTRATION NUMBER: 35,030
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TELECOMMUNICATION INFORMATION:
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TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2035 amino acids
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COUNTRY: United States
ZIP: 22313-1404
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Xaa Xaa which is the codon for Pro or Ala wherein Pro
CCC, CCA, or CCG; and Ala = GCT, GCC, GCA, or GCG."
                                                                                                                                                  /note= "The amino acids spanning 128 to 1899 constitute a repeated region wherein the 20 amino acids, 17 of which are fixed. The number of repeats varies from 1 to 40."
                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Amino acid 144 is Y = Xaa
which is the codon for Thr or Asn wherein Thr = ACT,
or ACG; and Asn = AAT or AAC."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 333 TTPKEPAPTTT-----KSAPTTPKEP------APTTTKEPAPTTPKEPAPTT 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --DNKPAPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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which is the codon for Pro or Ala wherein Pro
or CCG; and Ala = GCT, GCC, GCA, or GCG."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               374 TKE--PAPTTT-----KSAPTTPKEPAPTTPK----KPAPTTPKEPAPTTPKEPTTPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TKEPSPTTPKEPAPTT--TKSAPTTTKEPAPTT-----TKSAPTTPKEPSPTTK----E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     517 PAPTTPKEPAPTTPK----KPAPTTPKEPAPTTPK----EPAPTTTKKPAPTAPKEPAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           569 TPKETAP----TTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEBPTPTTPEEPAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAPDXRPXPGSTAPXAHGVTS----APDXRPXPGSTAPXAHGVTSAPDXRPX----PGST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.8%; Score 424.5; DB 4; Length 2035;
23.7%; Pred. No. 1.1e-18;
Live 69; Mismatches 511; Indels 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Amino acids 1 to 21 are a 21 amino acid precursor sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-KAETTTKGP--ALTTPKEP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 5.89
Best Local Similarity 23.71
Matches 255; Conservative
                                                                                                   NAME/KEY: Peptide
LOCATION: 128.1899
OTHER INFORMATION: 12
OTHER INFORMATION: 20
OTHER INFORMATION: 20
OTHER INFORMATION: re
FEATURE: Peptide
LOCATION: 134
OTHER INFORMATION: Xa
OTHER INFORMATION: Xa
OTHER INFORMATION: Xa
              STRANDEDNESS: single
TOPOLOGY: linear
                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 144
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Peptide
LOCATION: 147
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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CTHER INFORMATION:
CTHER INFORMATION:
US-09-083-116-2
                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Peptide
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Peptide
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679 530 727 585	773 644 817 702	863 762 919	979 868	1039 911	1098	e e
TPKAAAPNTPKEPAPTTPKEPAPTTPKETAPTTPKGT-APTTLKEPAP	KEPAPTTPKGTAPTTLKEPAPTTP	3 TTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAA			0 -PNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDXLPRVPNQGIIINPMLSD	9 ETNICNGKPVDGITT-LRNGTLVAFRGHYFWMLSPFSPPSPARRITEVWGIPSPID 1153
625 472 680 531	728 586 774 645	818 703 864	763 920 821	980	1040	. 1099 958
67 67 67 67	07 07 07 07	2 A A A	do yo	Oy Db	Qy	Oy Dp

Search completed: April 26, 2002, 16:26:24 Job time: 524 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

April 26, 2002, 16:32:49; Search time 114.61 Seconds (without alignments) 871.345 Million cell updates/sec Run on:

AA8 7064 1 MAWKTLPIYLLLLLSVFVIQ......ARAITTRSGQTLSKVWYNCP 1311

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES	
Result No.	Score	Query Match	Length DB	BB	. QI	Description
1	1078.5	15.3	3020	7	A43932	mucin 2 precursor,
7	950	13.4	1664	7	T18262	er i
m	855	12.1	1489	N	T31108	ч
4		11.4	1274	7	T16251	hypothetical prote
S.	798.5	11.3	1367	٦	S48478	glucan 1,4-alpha-q
9	784	11.1	1188	7	S49915	extensin-like prot
7	776.5	11.0	2187	7	T30826	nascent polypeptid
œ	672	9.5	1344	٦	A35175	mucin 1 precursor,
S	671	9.5	1151	~	T18535	$\overline{}$
10	662	9.4	1229	~	T25697	hypothetical prote
11	661	9.4	3507	~	T34513	
12	646.5		3570	7	T45025	
13	635.5		7962	N	I38346	i.
14	633	6	489	~	T11622	extensin class 1 p
12	632		191	N	C84672	hypothetical prote
16	630.5	ф.	066	~	I51618	nucleolar phosphop
17	626.5		971	~	T19431	hypothetical prote
18	625		6642	7	T29757	protein UNC-89 - C
19	622.5		839	~	F75518	hypothetical prote
20	0	9.0	801	~	T29018 ·	
21	607.5		924	~	S27923	gene LF3 protein -
22		9.0		N	S50125	larval glue protei
. 23	ഗ	7.9		~	S22456	hydroxyproline-ric
24	ഗ	7.9		~	T16543	hypothetical prote
25	526.5	7.9		~	S23760	polyphenolic adhes
26	S.	7.9	7	~	A53577	
27	554	7.8	a	~	T34434	hypothetical prote
28	551	7.8	620	7	67	olir
29	545	7.7	873	~	A47283	calphotin - fruit

hydroxyproline-ric extensin precursor	neurofilament trip hypothetical prote	exo-alpha-sialidas	hydroxyproline-ric	hypothetical prote vsaA protein precu	membrane glycoprot	membrane glycoprot	mucin FIM-C.1 - Af	mucin-like glycopr	interspersed repea	neurofilament trip
S20500 JU0465	QFMSH T27642	JH0557	J00985	T322/1 S70795	T45462 A37221	T45463	A45155	T31113	A54641	A43427
7 7	7	~ ~	0	N 61	7	~	~	7	~	7
369 416	1087	1162	328	1459 813	1072	867	662	1832	700	909
7.7	7.5	7.5	4.6	4.6	7.3	7.3	7.2	7.2	7.1	7.1
542 538.5	533 532	530.5	522	518	518 518	512.5	509.5	208	202	504.5
30	32 33	34 35	36	38	39	41	42	43	44	4 5

ALIGNMENTS

MASSILE INCREMENT INTESTIDAL - human (fragments) Na.Alternate names: nucles NSUC-41 Na.Alternate names: nucles NSUC-41 Na.Alternate names: nucles NSUC-41 C.Species: Home septems (man) N. Alternate names: A9963; A45106; B45106; A43932; B35332, A61257; P00128; P00128; N. Ancession: A49663; A401246; 1994 A. Title: Molecular cloning of human intestinal mucin (MUC2) CDNA. Identification of the Ancession: A49963; A101294132002 A. Ancession: A49963. A. Mocession: A49963; A101294132002 A. Ancession: A49963; A101294132002 A. Ancession: A49963; A101294132002 A. Title: The human MUC2 Annestinal mucin has cysteine-rich subdomains located both up Ancession: A49964 A. Residues: A1016; MULD: B9016075 A. Ancession: A4106 A. Anc
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encoding the cellulo
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C;Species: Clostridium thermocellum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T1826 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T1826 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Pujino, T; Bequin, P; Aubert, J.P.
                                                                                                                                                                                                                                                                                                                                       | 111:
| 111:--T 1886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VNP-------KSEDAGG-----AEGETPHMLL------RPHV 1020
                                                                                                    A;Residues: 1-1664 <FUJ>
A;Cross-references: EMBL:X67506; NID:q296879; PID:g296881; PIDN:CAA47841.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            849 ATTTEKTTESKITATTTQVTSTTTQDTTPFKITT---LKTTTLAPKVTTTKKTITTTEIM 905
  EPAPTIPKEPAPTTTKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAP 549
                                                                                                                                                                                                                                                                                                                                                                                                                       2289 CEPPPMPTCSNGLQPVRVEDPDGCCWHWECDCYCTGWGD-PHYVTFDGLYYSYQGNCTYV
                                                                                                                                                                                                                                                                                                                                                                                                  PTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTST-TSDKPAPTTPKETAPTTPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2184 YAPGEEVYNGTYGDICYFVNCSLSCTLEFYNWSCPSTPSPTPTPSK-STPTPSKPSSTPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      937 KPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPNQTPNSKLVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2243 KPTPGTKPPECPDFDPPR------QENETWWLCDCFM-ATCKYNNTVEIVKVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               789 AEPTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -TAKPKDRAINSKATTPKPOKPTKAPK
                                                                                                                                                                                                    1770 FSPFSTTTPTTPCVPLCNWTGWLDSGKPNFHKPGGDTELIGDVCGPGWAANISCRATMYP
                                                                                                                                                                                                                                                                                                                       629 PTTPKKPAPKELAPTT--TKEPTSTTSDKP----APT-TPKGTAPTTPKEPAPTTPKEPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAPTTPKKP-----APTTPETPPPTTSEVSTPTTTK-----EPTTIHKSPDESTPELS
                                                                                 TTPEELAPTTPEEPTPTTPEEPAPTTPKAAAPNTPKEPAPTTPKEPAPTTPKEPAPTTP~
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 950; DB 2;
Pred. No. 1.6e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: T18262
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: Minary;
A; Residues: 1-1664 <PUJ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: Z18847; MUID: 93209931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1021 FMPEVTPDMDYLPRVPNQGIIIN 1043
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31.0%;
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Best Local Similarity
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                                                                                                      A; Molecule type: mRNA
A; Residues: "T, 1952-1954 «JAN>
A; Residues: "T, 1955-1954 «JAN>
A; Residues: "T, 1955-1954 «JAN>
A; Experimental Source: bronchus
R; Xu, G; Huan, L.; Khatri, I.; Sajjan, U.S.; McCool, D.; Wang, D.; Jones, C.; Forstner, Biochem: Biophys. Res. Commun. 183, 821828, 1992
A; Title: Human intestinal mucin-like protein (MLP) is homologous with rat MLP in the C-t A; Reference number: PQ0328; MUID:92198477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        von
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        factor type A repeat homology;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1421
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                                                                                                                                                                                                                                                                                                                                                                                                                       A.Gene: GDB.MUC2
A.Cross-references: GDB:120203; OMIM:158370
A.Map position: 11p15.5-11p15.5
C.Superfamily: von Willebrand factor; von Willebrand factor type A repec; Keywords: glycoprotein; intestine; tandem repeat
F;2766-2834/Domain: von Willebrand factor type C repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --SFERGRECD------CDAQCKKYDKCCPDYESFCAEVKDNKKNRTKKK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 3020;
J. Clin. Invest. 87, 77-82, 1991
A;Title: Human bronchus and intestine express the same mucin gene. A;Reference number: A61257; MUID:91086481
A;Accession: A61257
A;Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.3%; Score 1078.5; DB 2; 28.1%; Pred. No. 9.1e-39; tive 88; Mismatches 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCNCDY -- NCOHYMECCPDFKRVCTAELSC -- -- -- --
                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 2328-2468
A; Cross - references: GB: MB6523
A; Experimental source: small intestine
A; Accession: P00329
A; Molecule type: protein
A; Residues: 2328-2342,'K', 2344-2354 <XUG1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 15.39
Best Local Similarity 28.19
Matches 378; Conservative
                                                                                                                                                                                                                                                A; Accession: PQ0328
                                                                                                                                                                                                                                                                                                                                                                                                            C; Genetics:
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smatches 361; Indels 230; G	PASTTPKEPTPTTIKSAPTTPKEPAPTT		-PTTTKEPAPTTTKSAPTTPKEPAPTTPK	PTPSDEPTPSDEPTPSETPTDTP	PAPT-TPKEPAPTAPKKPAPTTPKEPAP	PTPSETPEEPIPTOTPSDEPTPSDEPTP	-APTITKEPAPITIKSAPITPKEPS	DEPTPSDEPTPSDEPTPSDEPT	PKEPAPTTPKEPAPTTKKPAPTAPKEP	EKPAPT TPEELAPTTPEEPTPT - TP	OEPTPSDEPTPSD-EPTPSETP	TPKEPAPT-TPKETAPTTLK -	SOEFIFORIPERFIFED	APTTPKGTAPTTPKEPAPTTPKEPAPTT	GPTSTTSDKPAPTTPKETAPTTPKE	·PTDTPSDEPTPSDEPTPSD · EPTPSDE	PTTIHKSPDESTPELSAEPTPKALENS	JERTTPETTTAAPKMTKETATTTEKTTE	: : : KVTTTKKTITTEIMNKPEETAKPKDR :	TPSTTPTSG	TPKPQKPTKAP-KKPTSTKKPKTMPRVRKPKTTPTPRKM GGGTVPTSPTPTSKPTSTPAPTEIEEPTPSDVPGAIGGEHRA		: : : ::: : AKLLGADESYGAQSASPYSD			LVAFRGHYFWMLSPFSPPS	SQYWRFTNDIKD 1132
312; Conservative 104; Misma	VLAKPTP-KAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTIKSAPTTPKEP	VVIQPAPIKAASDEPIPTDTPSDEPTPS	TKSAPTTPKEPAPTTTKEPAPTTPKEPA	EPTPSETPEEPIPIDTPSDEPTPSDEPTPSDEPTPSDEPTPSETPEEPIPTPTP	KPAPTTPKEPAPTTPKEPAPTTKEPAPT-TPKEPAPTAPKKPAPTTPKEPAP	SDEPTPSDEPTPS DEPTPS DEPTPS SDEPTPSETPEET PTDTPSDEPTPSDEPTP	TTPKEPAPTTTKEPSPT-TPKEPAPTTTKS-APTTTKEPAPTTTKSAPTTPKEPS	DEPTPSDEPTPSETPEEPIPTPSET		APTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPT	TPSDEPTPSETPEEPIPTDTPSDEPTPSDEPTPSDEPTPSD-EPTPSETP	EEPAPITEKAAAPUTPKEPAPITPKEPAPITPKEPAPI-IPKETAPITPKGTAPITLK EET 1		EPAPTTEKKPAFKELAPTTTKEPT-STISDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTT : : : : : :	PKGTAPTTLKEPAPT-TPKKPAPKELAPTTTKGPTSTTSDKPAPT	- DEFIFSDEPTESETPEEPT	PAPTTPKKPAPT-TPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENS	PKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTE	SDEPTPSDEPTPSETPEEPIPTDTPSDEPTPSD-	₽	SKIRSDERIRSETREEPTPTITPTPTPSTT-	ATNSKATTPKPQKPTKAP-KKPTSTKKPKTMPRVRKPKTPTPRKM :	TSTMPELNPISRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHM	YLRGYPDGSFRPERNITRAEAAVIF	LLRPHVFMPE		IINPMLSDETNICNGKPVDGLTTLRNGT 	PARRITEVAGIPSPIDTVFTRCNCEGKTFFFKDSQYWRFTNDIKD
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Cyst germination specific acidic repeat protein precursor - Phytophthora infestans C;Species: Phytophthora infestans (potato late blight agent)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C;Accession: T31108
B;Goernhardt, B.
A;Reference number: 22986
A;Reference number: 22986
A;Reference number: 22988
A;Accession: T31108
A;Actus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Sestiues: 1-1489 <GGE>
A;Cross-references: EMBL:AF061185; NID:93851513; PID:93851514; PIDN:AAC72308.1
A;Genetics:
A;Genetics: 51; 135 NGDFKVTTPDTSTT-----QHNKVSTSPKITTAKPINPRPSLP-------P 173 174 NSDT----SKETSLTVNKETTVETKETTT---TNKQTSTDGKEKTTSAKETQSIEKTSAK 226 | || || || || || || || || || || || || EETTYAPAEETPYEPTTYAPTEETTYAPTEETT 1070 Gaps 78 FERGRECDCDAQCKKYDKCCPDYESFCAEVKDN---KKNRTKKKPTPKPPVVDEAGSGLD 134 301 YEPSDETEAPTEGTTY---VPREETTAAPSEDTTYAPREVTPYAPTEKPYDVEETTYVTE 357 417 477 286 533 337 ----TPKEPAPTTPKKPAPTTPKEPAPTTPKEPTTPKEP------AP--- 376 652 462 TTKEPAPTTPKEP-----APTAPKKPAPTTPKEPAPTTPKEPAPT--TTKEPSPTTPKE 428 PTEETTYAPTEETTYAPTEETMYAPIEETTYGPTEETTYAPTEATTYAPTEETPYAPTEE 772 TTKEP-----APTTPKEPAPTTPKKPAPTTPKEPAPT--TPKEPAPTTTKKPAPTAPKE 514 571 890 611 TAPTTPKGTAPT--TLKEPAPTTPKKPAPK-ELAPT--TTKEPTSTTSDKPAPTTPKGTA 665 701 KKP-----APKE---LAPT--TTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPA 750 358 ESTYAPTKSETNAPTERMHYAHIEKPCDTEVTMYAPTEETTYAPTEETTYAPTEETTYAP DLAPTSKVLAKPTPKAETTTKGPALTTPKEPTTTPKEPASTTPKEPTTTKEPTTTKSAPTTPK PIEETTYAPTEETTYAPAEETPYEPTEETTYAPTEETTYAPTEETTYAPTEE EPAPT-TIKSAPTIPKEPAPT--TIKEPAPTIPKEPAPTITKEPAPTITKSAPT-----P----APT-TTKSAPT------TTKEP-----APT-TTKSAPT--TPKEPSPT -----APT-----TPKAAAPNTPKEPAPTTPKEP-----APTTPKEPAPTTPKE PAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPT--TPEEPTPTTPEEP-Indels 228; Length 1489; Query Match 12.1%; Score 855; DB 2; Le Best Local Similarity 31.8%; Pred. No. 1.6e-29; Matches 362; Conservative 52; Mismatches 496; PTTPKEPAPTTPKEP-----APTTPKGTAPT-----227 338 593 377 713 463 515 653 429 833 572 951 1011 702 õ g ò g ŏ 셤 q g q οy ð Qγ à g ò qq δ g qq ò ò 合 ŏ g ŏ

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glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - yeast (Saccharomyces cerevisiae)
N;Alternate names: extracellular glucoamylase; mucin-like protein MUC1; protein XiAlternate names: extracellular glucoamylase; mucin-like protein MUC1; protein X;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 12-Nov-1999
C;Accession: 548478; A26877; B26877; S27281; JC6123
R;Rowley, K.
Submitted to the EMBL Data Library, October 1994
A;Reference number: 548478
A;Accession: 548478
A;Accession: 548478
A;Accession: S48478
A;Accession: Balanca, No. Fukui, S.
J; Bacteriol. 169, 2142-2149, 1987
A;Title: Gene fusion is a possible mechanism underlying the evolution of STAL
A;Reference number: A91831; MUID:87194600
A;Accession: A26877
A;Accession: Accession: Accession:
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A;Residues: 1-242 <YRAM>
A;Cross-references: EMBL:M16164; NID:9172522; PIDN:AAA35014.1; PID:9172525
A;Accession: B26877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           K-KEPEKPKD-APKVAAKPRDPSPKKAVPE--KEPAKVAAKPRDLSPKKAIPIPANTQEA 974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPT-TTKEPTSTTSDKPAPTTP 661
                                                                                                                                                                                                                                                                                                                                                                                                 KGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPT-----TPKKPAP----KEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             753 TPETPPPTTSEVSTPTTTKEPTTHKSP----DESTPELSA-EP---TPKALENSPKEPG
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                                                                                                                                                                                                                                                                                PTTPEELAPTTPEEP----TPTTPEEPAPTTPKAAAPNTPKEPAPTTPKEPAPTT-PKE
                                           PEKK-TPVLAKKAPTKPDSEAAADPVSGPSSKDPKLAKKAPVKPRDPSPMKAVPIKPAPK
                                                                                                                                                                                                                                              TPKEPAPTITKKPAPTA-PKEPAPTIPKETAPTIPKKLIPTTP-----EKLAPTIPEKPA
                                                                                                                          TTKEPAPTTTKSAPTTP-KEPSPTTKEPAPTTPK--EPAPTTPKKPAP--TTPKEPAPT
         --SPTTPKEPAPTTTKSAPT
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               APTAPKKPAP - - - - - TTPKEPAPTTPKEPAPTTKEP
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1244 ADFTMPAPKKPDTEDP 1259
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C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
C;Accession: T16251
R;Leimbach, D.
Submitted to the EMBL Data Library, January 1996
A;Pescription: The Sequence of C. elegans cosmid F35A5.
A;Reference number: 218485
A;Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56;
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                                                                                                                                                                                                                                                                                                                            KITATITQVISTITQDIT------PFKITT----LKTITLAPKVITIKKIITIEIM 905
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                                                                                                                       --VPTTKTPAATKPEMTTTAKDKTTERDLRTTP----ETTTAAPKMTKETATTTEKTTES
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Best Local Similarity
Matches 290; Conserv
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extensin-like protein - maize
C; Species: Zea mays (maize)
C; Species: Zea mays (maize)
C; Species: Zear-1995 #sequence_revision 12-May-1995 #text_change 29-Oct-1999
C; Accession: S49915
R; Rubinstein, A.L.; Broadwater, A.H.; Lowrey, K.; Bedinger, P.A.
Submitted to the EMBL Data Library, June 1994
A; Description: Pex genes: pollen-specific genes with extensin-like domains.
A; Reference number: S49915
A; Status: preliminary
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-1188 <RUB>
                                                                                                                                                                                                                                                                                                                   965 TIVPTITITSVITSSTITITITVCSTGINSAGETISGCSPKIITITVPCSTSPSETA--- 1021
                                                                                                                                                                                                                                                                                                                                                                                                                   PRKMTSTMPELNPTSRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRP 1018
                                                                                                                                                                                                                                                                                                                                                                                                                                               P--SVITVINFIPIT-ITTIVCSTGT------NSAGETISGCSPKIVTTVPC 1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1019 HVFMPEVTPDMDYLPRVPNQGIIINPMLSDETNICNGKPVDGLTTLRNGTLVAFRGHYFW 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1121 STGTGEYTTEATTLVTTAVTTTVVTTESSTGTNSA-GKTTTGYTTKSVPTT----YVT 1173
                                                                                                                                                                               SSSAPVPTPSSSTTESSVAPVPTPSSSSNITSSAPSSTPFSSSTESSSVPVPTPSSSTTE 848
                              636 APKELAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAP---TTPKEPAPT-TPKGTAPT 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: EMBL: 234465; NID: 9600117; PIDN: CAA84230.1; PID: 9600118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 PTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRPSL----PPN 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDTSKETSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKV 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----LAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAPTTPKEPA 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPPPPVKSPPPPABVGSPPPPEKSPPPAPVASPPVKSP--PPPTLVASPPPVKSPP 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTTTKSAPTTP--KEPAPTTTKEPAPTTPKEPAPTTTKEPAPTTTKSAPTTP-KEPAPTT 346
                                                     TESSSAPVPTPS-SSTTESSSAPVTPSSTTESSSAPVPTPSSSTTE
                                                                                           TLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAP-----TTP
                                                                                                                                                                                                                                                                                    862 AT--TIQVTSTTTQDTTPFKITTLKTTTLAPKVTT---TKKTITTT-EIMNKPEETAKPK
                                                                                                                                                         KKPAPTTPETPPPTTSEVSTPT----TTKEPTTIHKSPDESTPELSAEPTPKALENSPK
                                                                                                                                                                                                                       EPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKIT
                                                                                                                                                                                                                                            ----TKAPKKPTSTKKPKTMPRVRKPKTTPT
                                                                                                                                                                                                                                                                                                                                                                                    ----SESTITSPITPVTTVVSTTVVTTEYSTSTKPGGEITTTFVTKNIPTTYLTIAPT
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Similarity 29.9%; Pred. No. 1.3e-26;
30; Conservative 59; Mismatches 359; Indels. 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1079 MLSPFSPPSPARRITEVWGIPSPIDTVFTRC----NCEGKT 1115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  916 DRATNSKATTPKPQKP------
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Best Local Simil
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                                      50;
                                   NID:9172523; PIDN:AAA35015.1; PID:9172526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139 KVTTPDTSTTQHNKVSTSPKITTAKPINP-----RPSLPPNSDTSKETSLTVNKETT 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DCDAQCKKYDK---CCPDYESFCAEVK-DNKKNRTKKKPTPKPPVVDE--AGSGLDNGDF 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 DLSTGCNNYDNOGHSQTDFPGFYWNIDCDNNCGGTKSSTTTSSTSESSTTTSSTSESSTT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           234 TSSTSESSTITSSTSESSISSSTTAPATPITISCTKERPTPPITISCTKEKPTPPHHDTT 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191 VETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETT--TKG 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TPKEPAPTTTKEPAPTTPKEPAPTTTKEPAPTTTKSAPTTPKEPAPTTPKKPAPTTPKEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APTTPKEPTP----TTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAP----TTPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               468 AP----TTPKEPAPT-TPKKPAPTTPKEPAPTTPKEPAPTTTKKPAPTAPKEPAPTTPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         523 TAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPT-TPEEPTPTTPEEPAP----TTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    412 EPAPITIKEPSPITPKEPAPITIKSAPITIKEPAP----TITKSAPITPKEPSPITKEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 508 SSAPVPTPS-SSTTESSSAPAPTPSSSTTESSSAPVTSSTTESSSAPVPTPSSSTTESSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                577 KAAAPNIPKEPAPITPKEPAPTIPKEPAPITPKETAPI-TPKGTAPTLKEPAPTTPKKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 1367;
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11.3%; Score 798.5; DB 1; Length 1
Best Local Similarity 27.9%; Pred. No. 3.7e-27;
Matches 313; Conservative 108; Mismatches 523; Indels
A;Molecule type: DNA
A;Residues: 762-1331 <YA2>
A;Cross-references: EMBL:M16165;
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LATSIPKVTSPSPQKTPKSVS TTTKGPALTTPKEPTPTPKE : HVPPTSPPKSPVSDTLSG	QY 265 PASTIPKEPTPTIKSAPTTPKE-PAPTITKSAPTTPKEPAPTITKEPAPT 314	QY 315 TPKEPAPTTTKEPAPTTTKSAPTTPKEPAPTTPKK-P 350 	QY 351 APTTPKEDAPTTPKEPAPTTREPAPTTREPAPTTPKEPAPTAPKKPAPTTPKEPAP- 407 QY 351 APTTPKEPAPTTPKEPAPTTPKEPAPTTFFEPAPTAPKKPAPTTPKEPAP- 407 DD 1080 KTAGPKETPPGGVTAVPPEISLPPKETPQNATPNESLAASSQKRSPKTSVPKETPPG 1136	QY 408TTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTT-KSAPTTPK- 457	QY 458PAPTTREPAPTTPKEPAPTTPKRPAPTTPKEPAPTTP 496			OY 600 PKEPAPITPKETAPITPKGTAPITLKEPAPITP	QY 640 LAPTITKEPTSTISDKPAPTIPKGTAPTIPKEPAPTIPKE-PAPTIPKGTAPTT 692 1	QY	QY 753 TPETPPPTTSEVSTPTTKEPTTIHKSPDESTPELSAEPTPKALENSPK 801	QY 802 E-PGVPTTKTPAATKPEMITTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKI 860	QY 861 TATTTQVTSTTQDTTPFKITTLKTTTTLAPKVTTTKKIITTTEIMNKPEETAKPKDRATN 920	QY 921 SKATTPKPQKPTKAPKKPTSTKKPKTTPTPRKHTSTMPELNPTSRIABAML 980 activ	Qy 981 QTTTRPNOTPNSKLVEVNPKSEDAGGAEGETP 1012 	RESULT 8 A35175 mucin 1 N.Alternate names: breast carcinoma associated DF3 antigen; core protein KP39; episia ncreatic mucin; polymorphic epithelial mucin (PEM) N.Contains: mucin 1 precursor, epithelial tumor antigen splice form; mucin 1 precurso
DD 600 PPAPVASPPPPVKSPPPPTPVASPPPPAPVASSPPPMKSPPPPTPVSSPPPPEKSPPPPP 659 OY 347 PKKPAPTTPKEPAPTTPKEPTPTTPKEPAPTKEPAPTTPKEPAPTAPKKP 397 O	398	458 EPSPTTTKEPAPTTPKEP	518	5 5 5 88 5 5 86 5	624	670	OY 729 -TPKETAPTTPKEPAPTTPETPPPTTSEVSTPTTTKEPTTHKSPDESTPEL 787 Db 1058 KSPPPAPISSPPPVKSPPPAPVSSPPPPVKSPPPAPVSSPPPPIKSPPPPAPVS 1115	788	ZOLT 7	T30826 nascent polypeptide-associated complex alpha chain, muscle splice form gp220 - mouse nascent polypeptide alpha-NAC protein N;Alternate names: alpha-NAC protein C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse)			A;Molecule 'type: Dra A;Residues: 1-2187 <yot> A;Cross-references: EMBL:U48363; NID:g1666688; PID:g1666689; PIDN:AAB18732.1 C;Genetics:</yot>	A;Gene: Naca A;Map position: 10 A;Introns: 24/1; 1996/1; 2024/3; 2050/3; 2099/3; 2142/3; 2183/3 A;Note: differential splicing converts alphaNAC into a tissue-specific DNA-binding acti.	Query Match 11.0%; Score 776.5; DB 2; Length 2187; Best Local Similarity 27.6%; Pred. No. 5e-26; Matches 290; Conservative 119; Mismatches 416; Indels 227; Gaps 48;	OY 98 PDYESFCAEVKDNKKNRTKKPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNK 152

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A; Gene: GDB:MUC1; PUM
A; Cross-references: GDB:120705; OMIN:158340
A; Cross-references: GDB:120705; OMIN:158340
A; Map position: 142-14423
A; Introns: 20/1; 62/3; 1165/3; 1184/2; 1230/1; 1270/3; 1320/3
A; Introns: 20/1; 62/3; 1165/3; 1184/2; 1230/1; 1270/3; 1320/3
C; Superfamily: Polymorphic epithelial mucin
C; Keywords: alternative splicing; duplication; glycoprotein; phosphoprotein; polymorp
F; 1-134/Product: mucin 1 amino-terminal non-repetitive
F; 1-23/Domain: signal sequence #link PREB #status predicted <SIGB>
F; 1-19, 29-32/Domain: signal sequence #link PREB #status predicted <SIGB>
F; 1-19, 29-12, 1033-1344/Product: mucin 1 precursor, splice form B #status predicted <PREB>
F; 1-19, 29-12, 1033-1344/Product: mucin 1 precursor, splice form B #status predicted F; 1143-1344/Region: 20-residue repeats (GSTAPPAHGYTSAPDTRAP)
F; 1143-1344/Region: 20-residue repeats (GSTAPPAHGYTSAPDTRAP)
F; 1245-1272/Domain: transmembrane #status predicted <PREMS
F; 1066,1064,1118,1144,1222/Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 1213/Binding site: phosphate (Tyr) (covalent) #status predicted
                                                                                                  A;Note: undetermined tyrosine residues in the carboxyl-terminal non-repetitive region C;Comment: This protein is length polymorphic. Individuals may have between 21 and 12 partial repeats. The repeat shown is defined by Smal nuclease sites. C;Comment: Serine and threonine residues in the tandem repeat domain are extensively C;Comment: For an alternative splice form without a tandem repeat domain, see PIR:S48 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 LIVNKETTVETKETTTNK--QTSTDGKEKTTSAKETQSIEKTSAKD-LAPTSKVLAKPT 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 PGSGSSTTQGQDVTLAPATEPASGSAATWGQDVTSVPRPALGSTTPPAHDVTSAPDNK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      641 APTITKEPTSTISDKPAP--TTPKGTAPTIPKEPAPTTPKEPAPTTPKG----TAPTILK 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          273 PTPTT-----IKSAPTTPKEPAPTTT-----KSAPTTPKEPAPTTTKEP-----A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248 ISAPDIRPAPGSIAPPAHGVISAPDIRPAPGSIAPPAHGVISAPDIRPAPGSIAPPAHGV
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                                            A;Reference number: S51026; MUID:95080414
A;Contents: annotation
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Best Local Similarity 27.88
Matches 310; Conservative
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A; Residues: 998-1011. ES', 1014-1017;1018-1032, 'T', 1034-1037;1038-1057 <MAS>
A; Resperimental source: gastric carcinoma cell
R; Zrihan-Licht, S.; Baruch, A.; Elroy-Stein, O.; Keydar, I.; Wreschner, D.H.
FEBS Lett. 356, 130-136, 1994.
A;Title: Tyrosine phosphorylation of the MUCl breast cancer membrane proteins cytokine
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Gaps

74

448

627

512

586 687 747 661 807 717 859

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hypothetical protein F16F9.2 - Caenorhabditis elegans
hypothetical protein F16F9.2 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: T5-oct-1999 #sequence_revision 15-oct-1999 #text_change 18-Feb-2000
C.Accession: T25697
R.Frulton, B.
R.BBL Data Library, August 1996
A.Bescription: The sequence of C. elegans cosmid F16F9.
A.Reference number: Z20071
A.Accession: T25697
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                                                                                                                                                                                                            LPSSPVASAMHAKVTPRPLPASPVPMAASPASLGPDAARVALATNAASPGAKPEAAGGNG
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                                                                                   -TAGAVPKASTGTTPAAAPQQPVP---KAAPVTPPSPQQAVPRAATAAA----APVTPQQ
                                                                                                                                                                                                                                                                                                                           -PTTP-----KAAAPNTPKE----
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P----APTTPKEPAPTTPKKPAPTTPKEPAP-----TTPKEPAPT-TTKKPAPTAP
                                                 EPAPTTPKEPTPTT----PKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAPTTPKE
                                                                                                                                                     PVTKAATITINATPPPQPIPKAATITITATPVTPQQPIPKAGTDAAPPPAVPKAPSDGRAAT
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high molecular mass nuclear antigen - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 15-oct-1999 #sequence_revision 15-oct-1999 #text_change 15-oct-1999
C;Date: 15-oct-1999 #sequence_revision 15-oct-1999 #text_change 15-oct-1999
C;Date: 15-oct-1999 #sequence_revision 15-oct-1999
R;Shimada, M.; Harata, M.; Mizuno, S.
J. Cell Sci. 110, 3031-3041, 1997
A;Title: A nuclear matrix-associated high molecular mass nuclear antigen, HMNA, A;Reference number: Z18955; MUD:9803440
A;Accession: T18535
A;Status: preliminary; translated from GB/EMBL/DDBJ
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-----ASAASPIVPKATAEATAVTAASQSAPKAATDAAAVTAA---SQSAPKATV-EV
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                                                                                                                                                                                  ESTPELSAEPTPKALENSPKEPGVPTTKTPAA-----TKPEMTTTAKDK---TTERD
                                                                                                                                                                                                                 TRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPD
                                                                                                                                                                                                                                                                                                                        TLKTTTLAPKVTTTKKTITTT--EIMNKPEETAKPKDRATNSKATTPKPQKPTKAPKKPT
                                                                                                                                                                                                                                                                                                                                                       SAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAP--GSTAPPAHG
                                                                                                                                                                                                                                                                                                                                                                                           STKKPKTMPRVRKPKTTPTPRKMTSTMPELNP----TSRIAEAMLQT-TTRP---NQTPN
                                                                                                                                                                                                                                                      LRITPETT-----TAAPKMIKETAITIEKTIESKITATITQVISITIQDITP--FKII
                                                                                                                                                                                                                                                                            KEPAPTTP------KKPAPTTPETPPPTTSEVSTPTTTKEPTT-----IHKSPD
              --APDTRPAPGSTAPPAHGVTSAPDTRP
                                               ----KKPAPKELAPTTKGPTSTTSDKPAP--TTPK----ETAPTTP
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                601 AP-PAHGVTSAPDTRPAPGSTAPPAHGVTS-
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Matches 284;
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;Residues: 1-1229 <ful> Cross references: EMBL:U67956; PIDN:AAB07691.1; GSPDB:GN00028; CESP:F16F9.2 Experimental source: strain Bristol N2; clone F16F9 :Genetics: Gene: CESP:F16F9.2 :Map position: X :Introns: 35/1; 361/1; 384/1; 482/2; 517/1; 971/1; 1021/2; 1179/3</ful>	Query Match 9.4%; Score 662; DB 2; Length 1229; Best Local Similarity 27.1%; Pred. No. 2.2e-21; Matches 314; Conservative 91; Mismatches 367; Indels 388; Gaps 54;	KYDKCCPDYESFCAEVKDNKKNRTKKKPTPKPPVVDEAGSG 132		LONGING TO THE STATEMENT OF THE STATEMEN		<pre>226 KDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAPTTP 285 1:11:::1</pre>	32	219 VEPSVSTLASEDETTVTAIAESTITVIAEVSTTTEEPTTTAESTTKKSTTKAPATTEEPT 278	7	o webandmedenang na	339 ATETPEVAKSEDKMILSKTAATETTQQTTEVTDGPEKETTKEPSPTTFKEPAPTT 433	SAPTTPKEPSPT	399 TSTASKESDGFHTILKLKVTTADSDSTESATTVKPFNEETTTKSHVVPKPTKKGTVKVTP 458	473 KEPAPITPKKPAPTIPKEP 491	459 KLELSFDEPTEIT-KAPHPGKLLEKKTYHFVLSDNFARYSEAKENDDYNHLDYNHYREAK 517			T 59	PTTPKGTAPTTLKEPAPTTPKKDAPKETAPTTPTT 62		PKEPAPTTPKGTAPTTLKEPAPTTP70	675 GIITTDEETTSTTSTTPEITSTKEIVTESAITQTSVSVVESSTPRQLPERWKAIVNKF 732	702KKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPT 736	7	7	793 TTQBETTTTTTTTTEKTTTEKPTTSESATTETTTSEPSTTEST 838
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	ò	871	TTQDTTPFKITTLKTTLAPKVTTFKKTITTTEIMNKPESTAKPK
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	δλ	971	PTSRIAEA 978
-	QQ	1040	DGSDKKIIDEAQPTDEIRRA 1059
	RESULT	11	
	hypot C; Spe	hetic	hypothetical protein 2K783.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans
	C; Dat	e: 25 essio)-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 nn: T34513
	R;Fav submi	tted,	A.; Vaudin, M. to the EMBL Data Library, August 1994
	A;Des A;Ref	cript	.ion: The sequence of C. elegans cosmid 2K783.
	A; Acc A; Sta	tus:	n: T34513 preliminary; translated from GB/EMBL/DDBJ
	A; Mol A; Res	ecule	: type: DNA :: 1-3507 <fav></fav>
	A; Cro A; Exp	ss-re erime	ferences: EMBL:U13646; PIDN:AAC24418.1; GSPDB:GN00021; CESP:ZK783.1 ntal source: strain Bristol NO: clone 22782
_	C;Gen A;Gen	etics e: CE	SP:2K783.1
	A; Map	posi	;
	3504/1	7	14/1; 40/2; 04/1; 130/3; 303/1; 381/1; 586/1; 605/1; 1175/3; 1207/1; 1409/
	Que	ry Ma t Loca	Query Match 9.4%; Score 661; DB 2; Length 3507;
	Mat	ches	or Simitatiny 23.0%; Fred. NO. b.be-21; 278; Conservative 173; Mismatches 459; Indels 300; Gaps 53;
	δλ	27	LSSCAGRCGEGYSRD-ATC67
	QQ	1781	MGSCGCKCMAGYTGDGATCIKIEEEPKSDKTACTDEWSRLCELEKKQCTVDEEEV 1835
	οy	89	
	qq	1836 1	PQCGACLPGHHPINGTCQSLQISGLCAQKNDCNKHAECIDIHPDSHFCSCPDGFIGDGMI 1895
	δλ	06	CKKYDKCCPDYESFCAEVKDNKKNRTKKRPTPKPPVVDEA 129
	qq	1896 (
	٥y	130	GSGLDN-GDFKVTTPDISTTQHNKVSTSPKITTAKPINPRPSLPPN 174
	og C	1956 1	
	Qγ	175	SDISKETSLIVNKETIV-ETKETITINKOTSIDGKEKTISAKETQSIEKTSAKDLAP 230
	qq	2015	SESPENSTSSSKSTTASETIVSSTPSESSSSEAPLISSPATTTEVITESSWKSTTPKEE 2074
	Οy	231 -	-TSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTFTIKS-APTTPKEP 288
	Db 2	2075 8	SSSEITVKLSSKSPEVTESSVKSSPSTPS-TTSQSVTSTVPETSKSTVLSSEAPVTSTSP 2133
	δλ	289 A	APTITKSAPTTPKEPAPTTKEPAPTTPKEPAPTTTKEPAPTTTKSAPTTPKEPAPTTPK 348

A; Residues: 1-3570 <des> A; Cross-references: EMBL: Z72496; NID:91834502; PIDN:CAA96577.1; PID:91834503 A; Experimental source: placenta C; Genetics: A; Gene: MUC5B</des>	9.2%; Score 646.5; DB 2; Length Imilarity 22.5%; Pred. No. 2.8e-20; Conservative 107; Mismatches 536; Indels	OY 64 CTAELSCKGRCFESFERGRECDCDAQCKKYDKCCFULE IUI 	TPDTSTTO	OY 150 HNKVSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETTVETKET 196 	KDLAPTSKVLAKPTP	K			OY 351 APTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPA 406 1	QY 407 PITPKEPAPTITKEPS		PTTPKEPAPT : PPPKVLTT	QY 479 TPKKPAPTTPKEPAPTTTKKPAPTAPK-EPAP517	QY 518 -TTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPEE 570	Oy 571 PAPTTPKAAAPNTPKEPAPTTPKEPAPT-TPKEPAPTTPKETAPTTPKGTAPT-T 623 Dy 1262 GFTATP-SSSPGTALTPPVMISTTTPTTRGSTVTPSSIPGTTHTATVLTTTTTVATGS 1320	QY 624 LKEPAPTTPKKPAPKELAPTTTKEPTSITSDKPAPTTPKGTAPT-667 :	Qy 668 TPKEPAPTTPKEPAPT
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STAPITLKEPAPTTPKKPAPKELAPITTKGPTSTTSDKPAPTTPKETA	PTTPKEP 741 		EQPLGLECRAQAQPGVPLRELGQVVECSLDFGLVCRNREQVGKFKMCFNYEIRVFCCNYG 1616	-APTTPKKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALE 797 	NSPKEPGVPITKIPAAIKPEMITIAKDKITERDLRITPEIT	PMATMSTIHPSSTPETTHTSTVLTTKATTTRATSSMSTPSSTPGTTWILTELTTAA 1789 TTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQKP 931	TTTAALPHGTPSSTPGTTWILTEPSTTATVTVPTGSTATASSTRATAGTLKVLTSTATTP 1849	TKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRP 986	NOTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNOGIIIN 1043 :- :-		PSSSPGTALTPPVWISTTTTPTTRGSTVTPSSIPGTTHTATVLTTTTVA 2015	TEVWGIPSPIDTVFTRCNCEGRT 1115 :	- human (fragment) no sapiens (man) 7-1998 #sequence_revision 29-May-1998 # 38346 Kolmerz, B 93-296, 1995	ns: giant proteins in char nmber: A57430; MUID:960263 38346	Status: preliminary; translated from GB/EMBL/DDBJ Molecule type: mRNA Residues: 1-7962 <res> Cross-references: EMBL:X90569; NID:g1017426; PIDN:CAA62189.1; PID:g1017427</res>	:N snces: GDB:127867; OMIM:188840 1: 2q31-2q31	Match 9.0%; Score 635.5; DB 2; Length 7962;
	735	742	557	742	798	1734	1790	932	987	044	1965	1093	RESULT 13 138346 elastic titin C;Species: Hon C;Date: 29-Ma, C;Accession: 3 K;Labelt, S:, Science 270, 2	e: T renc ssio	us: cule dues s-re	tics 1: GD 18-re posi	, in (1)

76 ESFERG-----RECDCDAQCKKYDKCCPDYE--SFCAEVKDNKKNR------TKKKPTP 121

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5843 PKVIKKPVIEKIEKTSRRMEEEKVQVTKVPEVSKKIVPQKPSRTPVQEEVIEVKVPAVHT 5902
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| : | | : | | : | | : | | 5903 KKWVISEEKMFFASHTEEEVSVIVPEVQKEIVTEEKIHVAVSKRVE------PPPKVPE 5955
                                                                                                                                                                                                                                                                                                  6015 KPVPEEKIPVPVAKKKEAPPAKVPEVQKGVVTEEKITIVTQREESP----PPAVPEIPKK 6070
                                                                                                                                                                                                                                                                                                                                                                                                                                      :| |
6128 VEEKRFVAEEKLSFAVPQRVEVTRHEVSAEEEWSYSEEEEGVSISVYREEEREEEEEEV 6187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6071 KVPEERK-PVPRKEEEVPPPPKVPA--LPKKPVPEEKVAVPVPVAKKAPPPRAEVSKKTV 6127
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6368 EKVSIEAPKREPQPIKEVTIMEEKERAYTLEEBAVSVQREEEYEEYEBYDYKEFEEYEPT 6427
                                                                                                                                                                                                              162 AKPINPRPSLPPNSDTSKETSLT---VNKETTVETKETTTTNKQTSTDGKEKTTSAKETQ 218
                                                                                                                                                                                                                                                                  EPTPTTIKSAPTTPKEPAP-----TTTKSAPTTPKEPAPTTTKEPA-PTTPKE 318
                                                                                                                                                                                                                                                                                                                                        319 РАРТТТКЕРАРТТТКЅАРТТРКЕРАРТТРККРАРТТР-КЕРАРТТРКЕРТРТ----- 370
                                                                                                                                                                                                                                                                                                                                                                                                             -----PKEPAPT 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     378 TK-----PKEPA-----PT 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          393 APKK-----PAPTTPKE--PAPTTPKEP-APTTTKEPSPTTPKE----PAPTTTKSAP 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----TTPKEPAPT--TPKKPAPT--TPKEPAPTTFKFPAPTA 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              597 РТТРКЕРАРТТРКЕТАРТТРКСТАРТТКЕРАРТТКЕРАРТТРККРАРКЕLAРТТТКЕРТSTT---- 652
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                                                  --- TPDTSTTQHNKVSTS-PKITT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   512 PKEPAPTTPKETAPTTPKKLTPTTPEK -----LAPTTPEKPAPTTPEELAPTTPEEPT
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                                                                                                                                                                                             219 SIEKTSAKDLAPT--SKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPAS-----TTPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 439 TTTKEP--APTITKSAP---TTPKEPSPTTTKE-------PAPTT-----
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                                                  ----KPPV---VDEAGSGLDNGDFKVT-
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Db 6828 EEEEFVPEEEVLPEVKPKVPVPAPVPEIKKKVTEKKVVIPKKEEAPPAKVPEVPK 6882	1.
QY 879 KITTLKTTILAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQKPTKAPKKP 938	582 NIPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAPKELA :
QY 939 TSTKKPKTMPRVRKPKT-TPTPRKMTSTMPELNPTSRIAEAMLQTTTRPNQT 989 :-	308 PSPSPPPPYYYKSPPPPSPSPPPPYYYKSPPPPSPSPPPPYYYKSPPPPSYYYKSPPPPYYYKSPPPPYYYKSPPPPYYYY- 642 PTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPK 1
QY 990 PNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNGGIIINPMLSDE 1049	DD 367KSPPPPBSPSPPPPYYKSPPPPSPPPPYYKSPPPPSPSPPPYYKSPPPPSP 422 QY 702 KKPAPKELAPTTTKGPTSTTSDKPAPTTPKEPAPTTPKEPAPTTPKRPAPTTPETPPP 759 L
QY 1050 TNICNGRPVDGLTTLRNGTLVAFR 1073 Db 7004PPAKGRTVLEEKVSVAFR 7021	4.23 SPFPPIVIASPPPPSPSPPPPPIIASPPPPPSPSPPPPPPPPPP
	C84672 hypothetical protein At2927380 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
extensin class 1 precursor - compea C;Species: Vigna unguiculata (compea) C;Date: 16.Jul-1999 #sequence_revision 16-Jul-1999 #text_change 17-Nov-2000 C;Accession: T11622; S54155	C;Accession: C846/2 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y M.; Koo, H.; Woffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
R; Arsenijevic-Maksimovic, I.; Broughton, W.J.; Krause, A. Mol. Plant Microbe Interact. 10, 95-101, 1997 A; Title: Rhizobia modulate root-hair-specific expression of extensin genes. A; Reference number: Z17301; MOID:97155574	Nature 402, 761-768, 1999 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A:Reference number: A84420; MUID:20083487 A;Accession: 684672
A;Accession: T11622 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA	A;Status: preliminary A;Molecule type: DNA A;Resiques: 1.761 <5TO>
A; Residues: 1-489 <ars> A; Cross references: BMBL: X91836; NID: 91015936; PIDN: CAA62943.1; PID: 91015937 A; Experimental source: sub_species Red caloona R; Experimental source: sub_species Red caloona R; Arsenijevic-Maksimovic, I; Broughton, W.J.; Krause, A.</ars>	A;Cross_references: GB:AE002093; NID:95306260; PIDN:AAD41992.1; GSPDB:GN00139 C;Genetics: A;Gene: At2927380 A;Map position: 2
Subjected to the man of root-hair specific extensins involved in rhizoblum/legume inte A; Description: A class of root-hair specific extensins involved in rhizoblum/legume inte A; Accession: S54155 A; Accession: S54155 A; Accession: S54155	Query Match Best Local Similarity 31.1%; Pred, No. 2-20; Matches 31. Consorvative 44 Microstope 254. Indels 82. Cans 33.
A; Molecule types: mRNA A; Residues: 326-489 <ar2> A; Cross-references: EMBL:X86030; NID:g791149; PID:g791150 C; Genetics:</ar2>	PTPKAETTTKGPALTTPKEPTPT-TPKEPASTTRKEPTTIKSAPTTPKEPAPTT 293
A; Gene: Ext26G C; Superfamily: hydroxyproline-rich glycoprotein C; Keyworda: glycoprotein; hydroxyproline E; I-23/Tomain: signal sequence #status predicted <sig> F; I-34/AROTENGIN: extensin class 1 #status predicted</sig>	OY 294 KSAPTTPKEPAPTTTKEPAP-TTTKEPAPTTTKSAPTTPKEPAPT 345
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ALIGNMENTS

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EMBL; M94132; AAA59164.1; --
MIM; 158370; --
InterPro; IPR00359; Cys_knot.
InterPro; IPR00350; EGF-like.
InterPro; IPR001400; GF_Cysknot.
InterPro; IPR001400; VWFC.
InterPro; IPR00140; VWFC.
InterPro; IPR00140; VWG.
PRINTS; PR00438; GFCYSKNOT.
SWART; SW00214; VWC; 2.
SWART; SW00216; VWD; 4.
PROSITE; PS00125; GGF_1; UNKNOWN_1.
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MEDLINE-9320931; PubMed-8458832;
Fujino T., Beguin P., Aubert J.-P.;
"Organization of a Clostridium thermocellum gene cluster encoding the cellulosomal scaffolding protein CipA and a protein possibly involved in attachment of the cellulosome to the cell surface.";
I Bacteriol. 175:1891-1899(1993).
I SUBUNIT: ASSEMBLED INTO MONO-LEXERED CRYSTALLINE ARRAYS.
I SUBCLIULAR LOCATION: CELL WALL.
I SIMILARITY: CONTAINS 4 S-LAYER HOMOLOGY (SLH) DOMAINS.
                         1789 TGWLDSGKPNFHKPGGDTELIGDVCGPGWAANISCRATMYPDVPIGQLGQTVVCDVSVGL
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Bacteria: Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
Clostridium.
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01-JUN-1994 (Rel. 29, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
CELL SURFACE GIXCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN
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PROTEIN 1).
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Pfam; PF00395; SLH; 3.
PROSITE; PS01072; SLH_DOMAIN; 2. SLH EMBL; X67506; CAA47841.1; -. S-layer; Signal; 178194 1664 763 191 363 565 763 1494 1565 1625 1646 AA; 207 409 607 1453 1495 1566 1626 Cell wall; DOMAIN DOMAIN SEQUENCE Query Match Best Local S Matches 312 CHAIN DOMAIN REPEAT REPEAT REPEAT REPEAT DOMAIN DOMAIN DOMAIN 293 805 349 920 408 1095 1254 461 569 626 1155 q Qγ q g ò δ a δ g g ò ò q ò ò g q ò

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CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL 1,4-LINKED ALPHA-D-GLUCOSE RESIDUES SUCCESSIVELY FROM NON-REDUCING ENDS OF THE CHAINS WITH RELEASE OF BETA-D-GLUCOSE.
SIMILARITY: TO S.POMBE SPBC215.13.
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                            STRAIN=SPX101-1C;
MEDLINE-89031230; PubMed=3141213;
Pardo J.M., Ianez E., Zalacain M., Claros M.G., Jimenez A.;
Pardo J.M., Ianez E., Zalacain M., Claros M.G., Jimenez A.;
Samilar Short elements in the 5' regions of the STA2 and SGA genes from Saccharomyces cerevisiae.";
FEBS Lett. 239:179-184(1988).
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800 PKEPGVPTIKTPAAT--KPEMITTAKDKTTERDLRTTPETTTAAPKMTKETATTEKTTE
                                                                                                                                                   1397 SGGSGGSGGGGGGGGTVPTSPTPTSTPAP---TEIEEPTPSDVPGAIGGEHRA
                                                                                                                SKITATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDR
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STRAIN=S288C / AB972;

Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,

Barrell B.G., Conock R., Copsey T., Dear S., Devlin K., Fraser P.

Churcher C.M., Connock R., Hant S., Hunt S., Jagels K., Jones P.

Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,

Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,

Walsh S.V., Whitehead S.;

Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
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TO 1-40G-1988 (Rel. 34, Last sequence update)
TO 1-70G-1988 (Rel. 31, Last sequence update)
TO 1-70G-1995 (Rel. 31, Last sequence update)
TO -AUG-2001 (Rel. 40, Last annotation update)
TO -AUG-2001 (Rel. 40, Last annotation update)
TO -AUG-2001 (Rel. 41, Last sequence update)
TO -AUG-2001 (Rel. 40, Last annotation update)
TO -AUG-2001 (
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SEQUENCE OF 1-242 AND 762-1331 FROM N.A.
MEDLINE=87194600; PubMed=3106330;
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EMBL; M16164; AAA35014.1; --
EMBL; M16165; AAA35015.1; --
EMBL; X13857; CAA32069.1; --
PIR; BA6877; A26877.
PIR; A4878; S48478.
SGD; S0001458; MUC1.
Hydrolass; Glycosidase; Polysaccharide degradation; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 GLUCCAMYLASE S1/S2.
67 SER/THR-RICH.
17 N-LIBKED (GLCNAC. . . ) (POTENTIAL).
136110 MW; 91C0062DBD61AA9D CRC64;
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Larity 27.9%; Pred. No. 4.2e-26;
Conservative 108; Mismatches 523; Indels 177;
TO S.POMBE SPCC285.13C.
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1367
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817
874
            SIMILARITY: SOME,
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1367 AA;
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Matches 313; Conserv
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861
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P15941, P15942; P13931; P17626; Q14128; Q16442; Q16437; Q9Y4J2;
P15941, P15942; P33931; P17626; Q14128; Q16442; Q16437; Q9Y4J2;
O1-JAPR-1990 (Rel. 14, Last sequence update)
O2O-MG22001 (Rel. 40, Last annotation update)
MUCIN 1 PRECURSOR (POLYMORPHIC EPITHELIAL MUCIN) (PEM) (PEMT)
(PISIALIN) (TUMOR-ASSOCIATED MUCIN) (CARCINOMA-ASSOCIATED MUCIN)
(TUMOR-ASSOCIATED EPITHELIAL MEMBRANE ANTIGEN) (H23AG) (PEANUT-REACTIVE URINARY MUCIN) (BREAST CARCINOMA-ASSOCIATED ANTIGEN
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                                                       692 TLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAP----TTP
                                                                                             789 SSSAPVPIPSSSTIESSVAPVPIPSSSSNIISSAPSSIPFSSSTESSSVPVPIPSSSITE
                                                                                                                                                           802 EPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKIT
                                                                                                                                                                                                                                                      905 YPGSQTETSVSSTTETTIVPTKTTTSVTTPSTTTITTVCSTGTNSAGETISGCSPKTVT
                                                                                                                                    747 KKPAPTTPETPPPTTSEVSTPT-----TTKEPTTIHKSPDESTPELSAEPTPKALENSPK
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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tumor mucin cDNA.";
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TISSUE-Breast carcinoma;
MEDLINE-90368715; PubMed-1697589;
Gendler S.J., Lancaster C.A., Taylor-Papadimitriou J., Duhig T.,
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MEDLINE-90368716; PubMed-2394722;
MEDLINE-BO368716; PubMed-2394722;
MEDLINE W.S. Batra S.K., QI W.-N., Metzgar R.S., F
"Cloning and sequencing of a human pancreatic identification of the control of t
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"Human epithelial tumor antigen cDNA sequences. Differential splicing TISSUE-Breast carrinoma;
MEDLINE-90276414; PubMed-2112460;
Hareuveni M., Tsarfaty I., Zaretsky J., Kotkes P., Horev J.,
Hareuveni M., Tsarfaty I., Zaretsky J., Keydar I., Mreschner D.H.;
"A transcribed gene, containing a variable number of tandem repeats,
codes for a human epithelial tumor antigen. cDNA cloning, expression
of the transfected gene and over-expression in breast cancer SEQUENCE FROM N.A.
MEDLINE-91097524; PubMed-2268309;
MEDLINE-91097524; PubMed-2268309;
Lancaster C.A., Peat N., Duhig T., Wilson D.,
Taylor-Papadimitriou J., Gendler S.J.;
"Structure and expression of the human polymorphic epithelial mucin gene: an expressed VNTR unit."; "A highly immunogenic region of a human polymorphic epithelial mucin expressed by carcinomas is made up of tandem repeats."; J. Biol. Chem. 263:12820-12823(1988). rearfaty I., Hareuveni M., Horev J., Zaretsky J., Weiss M., Jelsch J.M., Garnier J.M., Lathe R., Keydar I., Wreschner D.H.; Isolation and characterization of an expressed hypervariable gene coding for a breast-cancer-associated antigen."; Gene 93:313-318(1990). reverse MEDLINE-90276413; PubMed-2351132; Wreschener D.H., Hareuveni M., Tsarfaty I., Smorodinsky N., Horov J., Zaretsky J., Kotkes P., Weiss M., Lathe R., Dion A., Lalani E.-N., Wilson D.; human tumor-associated MEDLINE-90088473; PubMed-2597151;
Abe M., Siddiqui J., Kufe D.;
"Sequence analysis of the 5' region of the human DF3 breast Mucin mRNA expression in lung adenocarcinoma cell lines and MEDLINE-96183746; PubMed-8608966; Weiss M., Baruch A., Keydar I., Wreschner D.H.; Preoperative diagnosis of thyroid papillary carcinoma by re transcriptase polymerase chain reaction of the MUC1 gene."; Int. J. Cancer 66:55-59(1996). PARTIAL SEQUENCE FROM N.A. MEDLINE-88330762; PubMed-3417635; Gendler S.J., Taylor-Papadimitriou J., Duhig T., Rothbard Yu C.J., Yang P.C., Shew J.Y., Hong T.M., Yang S.C., Lee L.N., Luh K.T., Wu C.W.; Biochem. Biophys. Res. Commun. 173:1019-1029(1990). Biochem. Biophys. Res. Commun. 165:644-649(1989). may generate multiple protein forms."; Eur. J. Biochem. 189:463-473(1990). Peat N., Burchell J., Pemberton L., L. Molecular cloning and expression of polymorphic epithelial mucin."; J. Biol. Chem. 265:15286-15293(1990). Eur. J. Biochem. 189:475-486(1990) SEQUENCE FROM N.A. MEDLINE-91033045; PubMed=1688329; SEQUENCE OF 1-169 FROM N.A. MEDLINE-90088473; PubMed-2597151; MEDLINE=96181716; PubMed=8604237; SEQUENCE OF 1-109 FROM N.A. TISSUE-Thyroid; SEQUENCE OF 1-89 FROM N.A. tissues."; Oncology 53:118-126(1996). TISSUE-Breast carcinoma; [5] SEQUENCE FROM N.A. SEQUENCE FROM N.A. Burchell J.; TISSUE-Lung; tissue. Keydar

ISOFORM)

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                                                                                           ALTERNATIVE PRODUCTS: VARIOUS VARIANTS ARE PRODUCED BY ALTERNATIVE
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Pfam: PF01390; SEA; 1.
SMART; SM00200; SEA; 1.
PROSITE; PS50024; SEA; 1.
Glycoprotein; Signal; Cytoskeleton; Actin-binding; Transmembrane;
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MISSING (IN ISOFORM D).
MISSING (IN POLYMORPHIC EPITHELIAL
                                                                                                                TISSUE SPECIFICITY: ABERRANTLY EXPRESSED IN HUMAN EPITHELIAL TUMORS, SUCH AS BREAST CANCER.

PTM: HIGHLY GLYCOSYLATED (N-AND O-LINKED CARBOHYDRATES AND SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. . .) (POTENTIAL)
T -> TATTAPKPAT (IN ISOFORM B).
                                                                                                                                                      POLYMORPHISM: THE NUMBER OF REPEATS IS HIGHLY POLYMORPHIC. VARIES FROM 21 TO 125 IN THE NORTHERN EUROPEAN POPULATION. MOST FREQUENT ALLELES CONTAINS 41 AND 85 REPEATS. SIMILARITY: CONTAINS 1 SEA DOMAIN.
                                                                         SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. A SECRETED
                          TISSUE-Breast carcinoma; Buluwela L., Liu Q., Luqmani Y.A., Gomm J.J., Coombes R.C.; Buliwela L., Liu Q., Luqmani Y.A., Gomm J.J., Coombes R.C.; Submitted (OCT-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 x 20 AA TANDEM REPEATS.
SEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
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ALT_INIT.
ALT_SEQ.
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ALT_SEQ.
ALT_SEQ.
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                                                                                                                                                                                                                                                                                           EMBL; J05582; AAA60019.1; -.
                                                                                                                                                                                                                                                                                                     AAA35804.1;
AAA55806.1;
AAA53150.1;
CAA36478.1;
AAB517.1;
AAB59612.1;
CAA78972.1;
CAA78972.1;
                                                                                                                                                                                                                                                                                                                                                                                              AAA35757.1;
AAD14376.1;
AAA59874.1;
                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, S81781; AAD14376.1;
EMBL, S81781; AAD14369.1;
EMBL, M21868; AAA59874.1;
PIR; A35175; A35175.
PIR; B35175; B35175.
PIR; S10218; S10218.
GlycoSuiteDB; P15941; --
MIM; 113720; --
                SEQUENCE OF 1-46 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23
11255
11162
11186
1255
960
11151
975
1029
11055
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                                                                                         IS ALSO PRODUCED
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975
1029
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                                                                   CYTOSKELETON
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1187
81
1034
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Z17324;
Z17325;
                                                                                                                                                                                                                                                                                                                                    M61170;
X52229;
X52228;
                                                                                                                                                                                                                                                                                                                           J05581;
                                                                                                                                                                                                                                                                                                                                                                                                 M31823;
                                                                                                                                                                                                                                                                                                         M32738;
                                                                                                           SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIĞNAL
CHAIN
DOMAIN
TRANSMEM
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPTTTKEPTT-----IHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAATKPEM 818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TQDTTP--FKIITLKTTTLAPKVTTTKKTITT--EIMNKPEETAKPKDRATNSKATTPK 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     417 GVISAPDIRPAPGSTAPPAHGVISAPDIRPAPGSIAP----PAHGVISAPDIRPAPGSTA 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    676 TPKEPAPTTPKG----TAPTTLKEPAPTTP------KKPAPKELAPTTKGPTSTT 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 SAPDIRPAPGSTAPPAHGVISAPDIRPAPGSTAPPAHGVISAPDIRPAPGSTAPPAHGVT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            515
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                                                                                                                                                                                                                                                                                                                279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        467
                                                                                                                                                                                                                                         181 TSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKD-LAPTSKVLAKPT 239
                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     584 TRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAP-PAHGVTSAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   819 IITAKDKTTERDLRTTPETT-----TAAPKMIKETATTIEKTIESKITATTIQVTSTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----APTTPKEPAPTTPK----KPAPTTPKEPAPTTPK----EPAPTTTKKPAPTAPKEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PKA----AAPNTPKEPAPTTPK----EPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          473 PPAHGVISAPDIRPAPGSTAPPAHGVISAPDIRPAPGSIAP----PAHGVISAPDIRPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              628 APTTP------KKPAPKELAPTTTKEPTSTTSDKPAP--TTPKGTAPTTPKEPAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    516 APTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPTT
                                                                                                                                                                                                                                                                                                                                                                                                            16 TVLTV------VTGSGHASSTPGGEKETSATQRSSVPSSTEKNAVSMTSSVLSSHS
                                                                                                                                                                                                                                                                                                                240 P-KAETTTKGP--ALTTPKEP------TPTTPKEPASTTPKEPTTI---K
                                                                                                                                                                                                                                                                                                                                                                                     SAPTTPKEPAPTTTKSAPTTPKEPAPTTTKEP-----APTTPKEPAPTTTKEPAPTTTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                            334 SAPTTPKEPAPTTP-----KKPAPTTPKEP-----APTTPKEPTPTTP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----KEPAPTTKEP-----APTTPKEPAPTAPK----KPAPTTPKEPAPTTPK----E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAPITIKEPSPITPKEPAPIT----TKSAPITIKEPAPITIKSAPITPKEPSPITIKEP--
                                                                                                                                                                                                         460; Indels 234;
                                                                                                                                                                        Length 1255;
                                                         -> 0 (IN REF. 9).
-> T (IN REF. 3).
-> T (IN REF. 3).
5E28DFC4DE7D9A82 C.
                        (IN REF. 11).
(IN REF. 9).
                                                                                                                                                                      9.2%; Score 651; DB 1;
27.8%; Pred. No. 3.9e-20;
tive 72; Mismatches 460;
MISSING (IN SI
T -> A (IN RE
P -> Q (IN RE
P -> Q (IN RE
S -> T (IN RE
A -> T (IN RE
A -> T (IN RE
A -> T (IN RE
                                                                                                                      122072
                                                                                                                                                                              Query Match 9.29
Best Local Similarity 27.8
Matches 295; Conservative
                                              134
154
1021
1251
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                                               134
154
1021
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                                                                                                            QT-PNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIINPML 1046
POKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPN 987
                                                    P--GSTAPPAHGVISAPDIRP---APGSTAPPAHGVISAPDIRPA-------PG 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TANDEM REPEATS OF Y-K-[PA]-K-[LP]-[ST]-Y-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-91025829; PubMed-1367451;
Filpula D.R., Lee S.M., Link R.P., Strausberg S.L., Strausberg R.L.;
"Structural and functional repetition in a marine mussel adhesive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ADHESIVE PLAQUE MATRIX PROTEIN (POLYPHENOLIC ADHESIVE PROTEIN) (FOOT
                                                                                                                                                                STAPPAHGVTSAPDTRPAPGSTAPPAH------GVTSAPDNRPALGSTA----PPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mytilus edulis (Blue mussel).
Eukaryota, Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilus.
NCBI_TaxID=6550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PARTIAL SEQUENCE, AND POST-TRANSLATIONAL MODIFICATIONS.
MEDLINE-83135732; Pubmed-6298211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-P-[ST]
/; 6EA85312748CAACE CRC64;
                                                                                                                                                                                                                     1047 SDETNICNGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSPPS 1087
                                                                                                                                                                                                                                                                    956 HIVTSASGSASGSASTLVHNGTSARATTPASKSTPFSIPS 996
                                                                                                                                                                                                                                                                                                                                                                                                                           875 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X54422; CAA38294.1; ... InterPro: IPR002964; Adhesive_plaq. InterPro: IPR002965; P_rich_extensn. PRINTS; PR01216; ADHESIVEI. PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lotechnol. Prog. 6:171-177(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 875 AA; 100412 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN 1) (MEFP1) (FRAGMENT
                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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Q25460;
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56;
                                                   148 TQHNKVSTSPKITTAKPINP------RP--SLPPNSDTSKETSLTVNKETTVET 193
                                                                                                                      177
                                                                                                                                                                                                                   346
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                                                                                                                                                                                                                                                                                               293
                                                                                                                                                                                                                                                                                                                 396 KPA--PTTPKEPA--PTTPKEPA--PTTKEPS--PTTPKEPA-PTTKSAPTTTKEPA- 445
                                  Gaps
                                                                                                                                                                                                                                                                                                                                    501
                                                                                                                                                                                                                                                                                                                                                                                        TTTKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPE 561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             821
                                                                          1 TKHEPVYKPVKTSYSAPYKPPTYOPLKKKVDYRPTKSYPPTYG-SKTNYLPLAKKLSSYK
                                                                                                     194 KETTTTNKQTSTDG--KEKTT---SAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKG
                                                                                                                                                        249 PALTIPKEPTPTTPKE----PASTTPKEPTPTIKSAPTTP----KEPAPTTTKSAPTT
                                                                                                                                                                         300 PKEPAPTTTKEPA--PTTPKEPA-----PTTTKEPA-PTTTKSAPTTPK--EPAPTT
                                                                                                                                                                                                                            234 KAKPSYPPTYKAKPSYPPTYKAKPSYPPTYKAKPTYKAKPTYKAKPTYKAKPSYPPTYKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 458 KPT-----YPSTYKA----KPSYPASYKAKPSYPPTYKSKSSYPSSYKPKKTYPPTYK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            616 PKGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAPTT----PKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    822 AKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTSTTTQDTTPFKIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           882 TLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQKPTKAPKK---P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 778 TYKSKSIYPSSYKPKKTYPPT---YKPKLTYPPTYK------PKPSYPPSYKPKITYP
        Length 875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STYKLKPSYPPTYKSKTSYPPTYNKKISYPSSYKAKTSYPPAYKPTNR 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              939 TSTKKPKTMPRVRKPKTTPTP------RKMTSTMPELNPTSR 974
      DB 1;
    7.9%; Score 556.5; Ilarity 28.7%; Pred. No. 2e-16
Conservative 106; Mismatches
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  7.9%;
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               Similarity
Query Match
Best Local Simi.
Matches 272;
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ZAN_HUMAN
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MAM_2; 4.

PROSITE; PS50060;

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                                                                                                                                                                                                                                                                                                                                                                                                  zonadhesin gene (ZAN).";
Genomics 41:119-122(1997).
-i- FUNTION: BINDS IN A SPECIES-SPECIFIC MANNER TO THE ZONA PELLUCIDA
OF THE EGG. MAY BE INVOLVED IN GAMETE RECOGNITION AND/OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!-SUBDNIT: PROBABLY FORMS COVALENT OLIGOMERS.
-!-SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN, EXCLUSIVELY ON THE APICAL REGION OF THE SPERM HEAD (FW SIMILARITY).
-!-TISSUE SPECIFICITY: IN TESTIS: PRIMARILY IN HAPLOID SPERMATIDS.
-!-DOMAIN: THE MAM DOMAINS PROBABLY MEDIATE SPERM ADHESION TO THE
                                                                                                                                                                                                  Glockner G., Scherer S., Schattevoy R., Boright A., Weber J., Tsui L.C., Rosenthal A.; "Large-scale sequencing of two regions in human chromosome 7q22: analysis of 650 kb of genomic sequence around the EPO and CUTLI loci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gao 2., Harumi T., Garbers D.L.;
"Chromosome localization of the mouse zonadhesin gene and the human
                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
O9Y493; O00218;
20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20NADHESIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000561; BGF-like.
InterPro; IPR000998; MAM.
InterPro; IPR0009965; P_rich_extensn.
InterPro; IPR002919; TIL.
InterPro; IPR001907; YUE.
InterPro; IPR001007; VWFC.
InterPro; IPR001007; VWFC.
                                                                                                                                                                                                                                                                                                                                        TISSUE=Testis;
MEDLINE=97271566; PubMed=9126492;
                                                                                                                                                                         SEQUENCE OF 1-2379 FROM N.A. MEDLINE=99018118; PubMed=9799793;
                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 2338-2700 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pfam; pF02345; TILa; 4.
Pfam; PF00094; vwd; 4.
PRINTS; PR01217; PRICHEXTENSN.
SMART; SM00137; MAM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF053356; AAC78790.1; -.
                                                                                                                                                                                                                                                                                     Genome Res. 8:1060-1073(1998).
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SMART; SM00011; VWC_def; 3.
SMART; SM00216; VWD; 3.
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Pfam; PF01826; TIL; 4.
                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                           genes
                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNALING.
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32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTPTTPEEPAPTTPKAAAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPT 622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKET--A 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        398 APTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPK 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     164 PINPRPSLPPNSDTSKETSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKT 223
                                                                                                                                                                                                                                                                                                                                                                                          224 SAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPT-----PTT1 278
                                                                                                                                                                                                                                                                                                                                                                     445 PVKVLPELPPVSPVSS----TGPSETTGLTENPTISTK-------KPTVSIEKP 487
                                                                                                                                                                                                                                                                                                                             Indels 107; Gaps
                                                                66 X HEPTAPEPTIDE REPEATS (APPROXIMATE)
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                                                                                                                                                                                                                                                                                                          Length 2700;
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NNQKMA -> RAGPGP (IN REF. 1)
                                                                                                                                                                                                                                                                            293013 MW; 80E60CC0B12277B1 CRC64;
                                                                                                                                                                                 (GLCNAC. . .)
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                                                                                                                                                                         (GLCNAC. . .)
      Cell adhesion; Repeat.
                                                                                                                                                                                                                                                                                                           Query Match
7.9%; Score 555.5; DB 1;
Best Local Similarity 32.6%; Pred. No. 5.5e-16;
Matches 199; Conservative 64; Mismatches 240;
                                                                               (MUCIN-LIKE DOMAIN).
                                                                                                                                                                      N-LINNED GECNAC.
                                                                                                                                                    (GLCNAC.
                                                                                     (PARTIAL).
                                     (PARTIAL).
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N-LINKED (
N-LINKED (
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VWFD
       Transmembrane;
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NEFH OR NFH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24;
                                                                                                                                                                                                                                                                                                                                                                                                                         PTM: EXTENSINS CONTAIN A CHARACTERISTIC REPEAT OF THE PENTAPEPTIDE SER-PRO(4). THE PROLINE RESIDUE IS HYDROXYLATED AND THEN GLYCOSYLATED.
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2 X 7 AA TANDEM REPEATS OF T-H-R-H-A-P-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 AETTIK-GPALTTP--KEPTPTT----PKEPASTTPKE---PTPTTIKSAPTTPKEPAP 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291 TTTKSAPTTPKEP-----APTTTKEPAPT---TPKEPAPTTTKEPAPTTTKSAPTTPKE 341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterida I; Solanales; Solanaceae; Nicotiana.
                                                                                                                   01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-MAR-1992 (Rel. 21, Last annotation update)
EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).
                                                                                                                                                                                                                                                                                                            Weller B., Lamb C.J.;
Specific expression of a novel cell wall hydroxyproline-rich
glycoprotein gene in lateral root initiation.";
Genes Dev. 3:1639-1646(1989)
--- FUNCTION: HAS A SPECIALIZED STRUCTURAL FUNCTION, POSSIBLY
THE MECHANICAL PENETRATION OF THE CORTEX AND EPIDERMIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X13885; CAA32090.1; -
PIR; S06733; S06733.
Repeat; Cell wall; Glycoprotein; Signal; Structural protein; Hydroxylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONTAINS THE SER-PRO(4) REPEATS.
3 X APPROXIMATE TANDEM REPEATS.
641DD2278AB28524 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX
                                                                                                620 AA.
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                                                                                                PRT;
                                                                                                                                                                                        Nicotiana tabacum (Common tobacco)
                                                                                                                                                                                                                                                                                  STRAIN=CV. XANTHI; TISSUE=Leaf;
MEDLINE=90128263; PubMed=2612909;
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600 3
65406 MW;
                                                                                               STANDARD;
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                 967 PASCKSPRPS 976
735 PITPKEPAPT 744
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229
229
236
205
499
620 AA;
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                                                                                             EXTN_TOBAC
P13983;
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SEQUENCE
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| |-|----PSPSHGHAPPSGGHTPPRGQHPPSHRRPSPPSRHGHPPPPTTYAQPPPTTYS 193
                                                                                                                                                                               250 RHLPPSPRRQPQPPTXSPPPAYAQSPQPSPTYSPPPPTYSPPPPSPIYSPPPAYSPSP 309
                                                                                                                                                                                                                                                             310 PPTPTPTFSPPPPAXSPPPTTYSPPPTYLPLSSPIXSPPPPVXSPPPPPSYSPPPTYL 369
                                                                                                                                                                                                                                                                                                                   612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carden M.J.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M, AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER.
NF-H HAS AN IMPORTANT FUNCTION IN MATURE AXONS THAT IS NOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shneidman P.S., Carden M.J., Lees J.F., Lazzarini R.A.;
"The structure of the largest murine neurofilament protein (NF-H) as
Ervealed by CDNA and genomic sequences.";
Brain Res. 464:217-231(1988).
                                                        397 PAPTTPKEPAPTTPKEPAPTTTKEPSPTTPK---EPAPTTTKSAPTTTKEPAPTTTKS--
                                                                                                                                        452 ---APTTPKEPSPTTTKEPAPTTPKEPAPTTPKKPAPTTPKEPAPT---TPKEPAPTTK
                                                                                                                                                                                                                                                                                                      556 APTTPEEPTPTTPEEPAPTTPKAAAP---NTPKEPAPTTPKEPAPTTPKEPAPTTPKETA
                                                                                                                                                                                                                                                                                                                                                                                    613 РТТРКGТАРТТLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEP
                                                                                  KPAPT---APKEPAPTTPKETAPTTPKKL-TPTT-----PEKLAPTTPEKPAPTTPEEL
                                                                                                                                                                                                                                                                                                                                  482 PPPSPIYSPPPDQVQPLPPTFSPPPRRIHLPPPPHRQP---RPPTPTYGQPPSPPTFSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Julien J.-P., Cote F., Beaudet L., Sidky M., Flavell D., Grosveld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Sequence and structure of the mouse gene coding for the largest neurofilament subunit.";
Gene 68:307-314(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NFH_MOUSE STANDARD; PRT; 1087 AA.
P19246; Q61959;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 21, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    791 PTPKALENSPKEPGVPTTKTPAATKP 816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             599 PSP------PTTYSPPSPPP 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=SWISS WEBSTER; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-89121513; PubMed-3220257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=89089138; Pubmed=3145094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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38;
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                                                                                       PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTIONING OF THE LARGER NEDROFILAMENT POLYPEPTIDES (NF-M AND NF-H), THE LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND COINCIDENT WITH A CHANGE IN THE NEUGOFILAMENT FUNCTION. SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY. CAUTION: REP. 2 SEQUENCE DIFFERS FROM THAT SHOWN IN POSITIONS 534 TO 716 AND IS SHORTER DUE TO FRAMESHIFTS.
SUBSERVED BY THE TWO SMALLER NF PROTEINS.

PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P, NFH IS
PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIE. IT IS
FHOGHT THAT PHOSPHORYLATION OF NFH RESULTS IN THE FORMATION OF
INTERPLAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE
OF AXONAL CALIBER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEAGSGLDNGDFKVT----TPDTSTTQHNKVSTSPKITTAKPINPRPSLPPNSDTSKET 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 SLIVNKETTVETKETTTINKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPK 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            450 VIVEGOTEEIRVTEGVTEEEDKEAQGQEGEEAEEGEEKEEEELAAATSPPAEEAASPEKE 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TANDEM REPEATS OF K-S-P-A-E-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pfam; PF00038; filament; 1.
PROSITE; PS00226; IF; 1.
Intermediate filament; Coiled coil; Neurone; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.5%; Score 533; DB 1; Length 1087; 27.5%; Pred. No. 2.1e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COLL 2B.

COLL 2B.

K -> QA (IN REF. 2 AND 3).

S -> T (IN REF. 2 AND 3).

S -> T (IN REF. 2 AND 3).

L -> G (IN REF. 2 AND 3).

P -> PREAKSP (IN REF. 3).

G -> A (IN REF. 3).

G -> A (IN REF. 3).

T -> N (IN REF. 3).

T -> N (IN REF. 3).

T -> N (IN REF. 2 AND 3).

T -> N (IN REF. 2 AND 3).

MX; 57BAC76A38EDICB9 CRC64;
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; Mismatches 330;
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GLU-RICH (ACIDIC).
50 X 6 AA TANDEM F
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COIL 1A.
LINKER 1.
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                                                                                                                                                                                                                                                                                                                             EMBL; M24496; AAA39813.1; -...
EMBL; M24349; AAA39813.1; JOINED.
EMBL; M24494; AAA39813.1; JOINED.
EMBL; M24495; AAA39813.1; JOINED.
EMBL; M35131; AAA39809.1; ALT_FRAME.
EMBL; Z31012; CAA83229.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81;
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239
261
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843 84
1087 AA;
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PIR; A43778; A43778.
MGD; MGI:97309; Nfh.
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Best Local Similarity
Matches 216; Conserv
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492
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CONFLICT
SEQUENCE
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"The Trypanosoma cruzi neuraminidase contains sequences similar to batchrial neuraminidases, YWTD repeats of the low density lipoprotein receptor, and type III modules of fibronectin.";
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                                                                                                                                                                                                                                                                                                                                                                                                                   670 KEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPTT 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trypanosoma cruzi.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
                                                                                                                                                                                                          503
                                                                                                                                                                                                                         SPAAVKSPGEAKSPGEAKSPAEAKSPIEVKSPEKAKTPVKEGAKSPAEAKSPEK 789
                                                                                                                                                                                                                                                             563
                                                                                                                                                                                                                                                                                                              611
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01-NOV-1991 (Rel. 20, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
SIALIDASE (EC 3.2.1.18) (NEURAMINIDASE) (NA) (MAJOR SURFACE ANTIGEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----KKEEMPAAPEK-------KDIKEEKTIESRKPEEK----
                                                                                                                      TKSAPTTPKE-PSPTTTKEPA----PTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTT
                                                                                                                                                                                                                                                             TKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEP
                                                                                                                                                                                                                                                                                   790 AKSPVKEDIKPPAEAKSPEKA-KSPVKEGAKPPEKAKPLDVKSPEAQTPVQEEATVPTDI
                                                                                                                                                                                                                                                                                                              564 TPTTPEE-PAPTTPKAAAPNTPKEPAPTT----PKEPAPTTP-----KEPAPTTPKET
                                                                                                                                                                                                                                                                                                                                612 APTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSD--KPAPTTPKGTAPTTP
                                                                                                                                                                                                                                                                                                                                                                                  PKETAPTTPKEPAPTTPKKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSA
242 AETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAPTTPKEPAPTTTKSAPTTPK
                                                                                                                                                       P----APTTPKEPAPTTTKEPAPTTTKEPSPTTPKEPA----PTTTKSAPTTKEPAPTT
                   ---PITPKEPA----PITPKEP----TPTTPKEPAPTIKEPAPTTPKEPA----PTAPKK
                                                  EP-APTITKEPAPTIPKEPAPTITKEP----APTITKSAPTIPKEPA----PITPKKPA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-SILVIO X-10/4;
MEDLINE-91277609; Pubmed-1711561;
Percira M.E.A., Mejla J.S., Ortega-Barria E., Matzilevich D.,
Prioli R.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1162 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=5693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1083 TKGEK 1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTEK 854
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P23253;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34;
                                                                                                                                                                                                                                                                                                                                                                                                DEVELOPMENTAL STAGE: MAXIMAL ACTIVITY IN TRYPOMASTIGOTES, MINIMUM IN PPIMASTIGOTES AND NO DETECTABLE IN AMASTIGOTES.
MISCELLANEOUS: THE VARIABLE LENGTHS OF THE LONG TANDEM REPEAT DOMAIN COULD ACCOUNT IN PART FOR THE POLYMORPHISM OF THE TNCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPTTPKE-PASTTPKEPTPTIKSAPTTPKEPAPTTTKSAPTTPKEPAPTTFEPAPTTP 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          599 TPSTPADSSAHSTPSTPVDS---SAHSTPSTPADSSAHGTPSTPVDSSAHGT----PSTP 651
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                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FIRONECTIN TYPE-III.

44 X 12 AA TANDEM REPEATS, LTR DOMAIN.

N-LINKED (GLONG. . .) (POTENTIAL).

N-LINKED (GLONAC. . .) (POTENTIAL).

N-LINKED (GLONAC. . .) (POTENTIAL).

M: 07049221897C6A40 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO FAMILY 33 OF GLYCOSYL HYDROLASES. SIMILARITY: CONTAINS 3 BNR REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P29768; 1DIL.
InterPro; IPR002860; BNR.
Pfam; PF02012; BNR; 2.
Hydrolase; Glycosidase; Glycoprotein; Repeat; GPI-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYS-RICH.
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BNR 2.
BNR 3.
   MEDLINE=91376547; PubMed=1896773;
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                                                                                       trypomastigotes.
Trop. Med. Paras.
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DOMAIN
CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1085 DSSAH-STPAD-SSAHGTP--STPADSSAHSTP-----STPAGSSAN 1125
                                                                                                                                                           Martin J.H., Benzer S., Rudnicka M., Miller C.A.;
"Calphotin: a Drosophila photoreceptor cell calcium-binding protein.";
Proc. Natl. Acad. Sci. U.S.A. 90:1531-1535(1993).
                                                     643
                                                                                            644 TIKEPISITSDKPAPITPKGTAPTIPKE-PAPITPKEPAPITPKGTAPITLKEPAPTIPK 702
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                    STPVDSSAHSTPSTPADSSAHS-TPSTPVDSSAHSTPSTPADSSAHGT
TTP-EKLAPTTPEKPAPTTPEELAPTTPEE----PTPTTPEEPA----PTTP-KAAAPNT
                                                           PKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPT
                                                                                                                                          703 KPAPKELAPTTTKGPTSTTSDKPAPTTPK----ETAPTTPKEPAPTTPKKPAPTTPETPP
                                                                                                                                                                                         759 PITSEVSTPTITKEPTIIHKSPDESTP-ELSAEPTPKALENSPKEPGVPTIKTPAATKPE
                                                                                                                                                                                                                                                                                                                                                 01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-FFB-1994 (Rel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                               865 AA.
                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93165729; PubMed=8094559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L02111; AAA28405.1; -.
                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                               1126 GT 1127
                                                                                                                                                                                                                                        818 MT 819
                                                                                                                                                                                                                                                                                                                                                                                    CALPHOTIN.
CPN OR CAP.
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Q02910;
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 534
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CPN_DROME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    297 ETPALAPVVAESQVAANTVVATPPTPAPEPETIAPPVVAETPEVASVAVAETTPPVVPPV 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 535 TPEKL-APTTPEKPAPTTPEELAPTTPEEPTPTTPEEP---APTTPKAAAPNTPKEPAPT 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       591 TPKEPAPTTPKEPAPTTPKETAPTTP-KGTAPTTLKE-----PAPTTPKKPAPKE 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   414 V----LPPVAAEPVPAVVAEETPETPAPASAPVTIAALDIPEVAPVIAAPSDAPAEAPSA 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         470 AAPIVSTPP--TTASVPETTAPPAAVPTEPIDVSVLSEAAIETPVAPPVEVTTEVAVADV 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               528 APPEAAADLIIEPVEPPAPIPDLLEQTTSVPAVEAAESTSS--PIPETSLPPPNEAVASP 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            738 PKEPAPTTPKKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPD------ESTPEL 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 PVAATPTPVVQIPVAAPVIATPPVAASAPTPAAVTPVISPVIASPPVVPANTTVPVAAPV 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PKEPA---PTAPKKPAPTTPKEPAPTTPKE-PSPTTPKEPAP-----TTTKSA 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 AAVPAAVPVVAPVLAPAVAPAVAPAVAETPAPPPVAEIPVATIPECVAPLIPEVSVVATK 236
                                                                                                                                                                                                                                                                                                                             229 APTSKVLAKP-TPK---AETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAPTT 284
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           846 KETATTTEKITESKITATTTQVTST-----TTQDTTPFKITTLKTTTLA-PKVTTTKKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVAVAPITAPEPIP----EPEPSLATPTEPIPVEAPVVIQEAVDAVEVPVTETSTSIPET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              642 TVE-FPEAVAEKVLDPAI--TEAPVTTQEPDVANINDGAPATEI-TTPAVEIVTAAAEVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTTTKEP---APTTTKSAPTTPKEPSPTTTKEPA-PTTPKEPAPTTPKKPAPTTPKEPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAESIPAPVVATTPVPAT ---LAVTDPDVTASAVPELPPVIAPSPVPSAVAETPVDLAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAPITIKEPISITSDKPAPITPKGTAPTTP-----KEPAPITPKEP--APTIPKGTAPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      692 TLKEPA-----PTTPKKPAPKELAPTTT----KGPTSTTSDKPAPTT----PKETAPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLAAAEPVVVAPPATETPVVAPAAASPHVSVAPAVETAVVAPVSASTEPPVAAATLTTAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTP------KEPAPTTTKKPAPTAPKEP---APTTPKET-----APTTPKKLTPT
                                                                                                                                                                                                                                                                                                                                                                                   PKEPAPTTTKSAPTTP-KEPAPTTTKEPAPTTPKEPAPTTTKEPAPT----TTKSAPTTP
                                                                                                                                                                                                                                                                                                                                                                                                              VIIPAAPAIAAASVIPVASVAPPVVAAPIP-----PAASPVSIPVAVAQIPVAVSAPVAP
                                                                                                                                                                                                                                                                                                                                                                                                                                           340 KEPAPTTPKKPAP-----TTPKEPAPTTPKEPTP-----TTPKEPAPTTKEPAPTT
                                                                                                                                                                                                                                                                                                                                                       8 SPVSAPVAAPVTPSAVAAPVQVVSPAAVAP-----APAAPIAVTPVAPPPTLASVQPAT
                                                                                                                                                                                                                                                                                                    433; Indels 152;
                                                                                                                                                                                                                                                                       Length 865;
                                                                                                                                         5
                                                    A -> AV..

I -> T (IN b..

I -> Y (IN REF. -2).

T -> A (IN REF. 2).

VO -> AP (IN REF. 2).

VO -> AP (IN REF. 2).

A I -> V (IN REF. 2).

A I -> Y (IN REF. 2).

A I -> Y (IN REF. 2).

A I -> Y (IN REF. 2).

B -> T (IN REF. 2).

A I -> T (IN REF. 2).

B -> T (IN REF. 3).

B -> T (IN REF. 3).
                                                             (IN REF.
                                                                                                                                                                                                                                                                          ; DB 1;
2.4e-15;
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                                                                                                                                                                                                                                                                         7.5%; Score 530; DB 26.2%; Pred. No. 2.4e Live 73; Mismatches
                                                           36
43
43
43
43
43
64
70
100
5
1127
1154
1160
534
699
703
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703
                                                                                                                                                                                                                                                                                         Local Similarity 26.2 tes 233; Conservative
        AAA28420.1;
                      PIR; A47282; A47282.
FlyBase; FBgn0010218; Cpn
                                                                                                                                                                                                       703
721
865 AA;
                                                  Calcium-binding
                                                                                            CONFLICT
CONFLICT
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                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NONREPETIVE LINKER.
TANDEM REPEATS OF Y-K-[PS]-K-[IP]-[ST]-Y-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i TISSUE SPECIFICITY: PRODUCED BY THE BYSSAL GLAND.
-i DOMAIN: ALMOST EXCLUSIVELY COMPOSED OF REPEATS OF A DECAPEPTIDE.
-i PUM: PROLINES IN THE REPEAT ARE HYDROXYLATED (SINGLE OR DI-) AND
ALSO TYROSINE (THUS PRODUCING DOPA = 3,4-DIHYDROXYPHENYLALANINE).
DIAIPVIDPPVPQEIAVAEIPETDTKPAEVIVEQSTIPIEAPVPEVSKYAEPVISEAPAA 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Addresive protein cDNA sequence of the mussel Mytilus coruscus and "fadhesive protein cDNA sequence of the mussel Mytilus coruscus and its evolutionary implications.";
J. Mol. Evol. 43:348-356(1996).
-!- FUNCTION. PROVIDES ADHESIVENESS TO THE MUSSEL'S FOOT. MUSSELS PRODUCE ONE OF THE STRONGEST WATER INSOLUBLE GLUE. THE MUSSEL'S ADHESIVE IS A BUNDLE OF THREADS, CALLED A BYSSUS, FORMED BY A FIRROW COLLABOROUS CORE COATED WITH ADHESIVE PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŝ
                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ADHESIVE PLAQUE MATRIX PROTEIN PRECURSOR (FOOT PROTEIN 1) (MCFP1).
                                                    ITTTEIMNKPEETAKPKDRATNSKATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPKTTPT
                                                                                                      EVPITAGDNPDNTSVGISEVVPTIAEKPVEEVPTS-.EIPEQSSSPS--DSVPVAKITPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mytilus coruscus (Sea mussel).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.3%; Score 518.5; DB 1; Length 872;
29.2%; Pred. No. 7e-15;
tive 80; Mismatches 407; Indels 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inoue K., Takeuchi Y., Takeyama S., Yamaha E., Yamazaki F., Odo
Harayama S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADHESIVE PLAQUE MATRIX PROTEIN. NONREPETIVE LINKER.
                                                                                                                                                          PRKMTSTMPELNPTSRIAEAM---LQTTTRPNQTPNSKLVEVN-----PKS 1001
                                                                                                                                                                                           P-[PST]-[ST].
NONAPEPTIDE 1.
NONAPEPTIDE 2.
i; 98CC70D7C75FF3C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                   ΑĄ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR002964; Adhesive_plaq.
Interpro; IPR002965; P_rich_extensn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: SECRETED
                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Foot;
MEDLINE=96394686; PubMed=8798340;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR01216; ADHESIVEI.
PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal; Repeat; Hydroxylation SIGNAL 1 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101677
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                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20
872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=42192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21
21
124
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                                                                                                                                                                                                                                                                                                                                                         FP1_MYTCO
Q25434;
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SEQUENCE
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Best Local 9
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235
                                                                                             YPTKRYOPTYGSKTNYPPIYKPIAKKLSSYKAIKTTYPAYKAKTSYPPSYK-----HKIT 139
                                                                                                                                                                                           140 YPPTYK-----PKITYP--PTYKQKPSYPPSYKPKTTYPPTYK-----PKITYPPTYK 185
                                                                                                                                                                                                                                               SAPT-TPKEPAPT--TTKEPAPTTPKEPAPTTTKEPAPTTTKSAPTTPKEPAPTT--PKK 349
                                                                                                                                                                                                                                                                                 294
                                                                                                                                                                                                                                                                                                                                                PAPTTPKEPAPTT----PKEPTPTT--PKEPAPTTKEPAPTTPKEPAPT-APKKPAPTTP 402
                                                                                                                                                                                                                                                                                                                                                                                 KEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPT----TTKEPAPTTTKSAPTTPK 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          K-PKPSYPPTYKPKITYPPT-YKPKPSYPTPYKOKPSYPPIYKSKSSYPTSYKSKKTYPP 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPSPTITKEPA-PTTPKEPAPTTPKKP-APT-TPK------EPAPTTPKEPAPTTTKKP 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIYKPKITYPPIYK-----PKPSYPPSYRPKITYPPIYKPKIKYPPIYKPKASYPPIYK 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPAPTIPKEPAPTIPKGTAPTILKEPAPTIP----KKPAPKELAPTITKGPISITSDKPA 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTT--PKETAPTTPKEPAPTTPK--KPAPTTPET-----PPPTTSEVSTPTTKEPTT 775
                    84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       688 Y---PPSYKPKKTYPPTYK-----PKISYPPTYK----TKPSYPASYKRKTSYPPTYKPK 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQ---KPTKAPKKP-TSTKKPK-T 946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          827
VYGSAYSGASAGAYK-TLPGSHPYGSKHVPVYKPMNKIPT-PYI--SKKSYPAPYKPKGY
                                                 DISKETSLIVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKVL
                                                                                                                                            236 AKPTPKAETTTKGPALTTPKEPT-PTTPKEPASTTPKEPTPTTKSAPTTPKEPAPTTTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APTAPKEPAPTTPKETAP----TTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T-YKPKISYPPTYKPKASYVSSYKSKKTYPPTYKPKISYPPTYKPKPSYPPTYKPKITYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PT-PTIPEEPAPTTPKAAAPNTPK-EPAPTTPKEPAPTTP----KEPAPTT--PKETAP
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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T. P-domains as shuffled cysteine-rich modules in integumentary mucin c.1 (FIM-C.1) from Xenopus laevis. Polydispersity and genetic polymorphism.";

D. J. Chem. 267:24620-24624(1992).

I. J. Biol. Chem. 267:24620-24624(1992).

I. J. Biol. Chem. SCOULD BE INVOLVED IN DEFENSE AGAINST MICROBIAL INVECTIONS: COULD BE INVOLVED IN DEFENSE AGAINST MICROBIAL INVECTIONS: PROTECTS THE EPITHELIA FROM EXTERNATIVE BRODUCTS: A NUMBER OF DIFFERENT FORMS OF THE PROTEIN MAY BE PRODUCED BY ALTERNATIVE SPLICING.

I. TISSUE SPECIFICITY: SKIN.

TISSUE SPECIFICITY: SKIN.

TISSUE SPECIFICITY: SKIN.

TISSUE SPECIFICITY: SKIN.

TISSUE SPECIFICITY: SKIN. 8 X APPROXIMATE TANDEM REPEATS, THR-RICH. 2-1. 8 X 8 AA APPROXIMATE TANDEM REPEATS, ALA/THR-RICH. Amphibia; Batrachia; Anura; Mesobatrachia; Pipoldea; Pipidae; P-TYPE 2. P-TYPE 3. 12 X APPROXIMATE TANDEM REPEATS, THR-RICH. HSSP, P04002, MALD.
HSSP, P04002, MEA.
InterPro, IPR000519; P_trefoil.
InterPro, IPR00088; trefoil; 6.
SMARY, SM00018; P: 6.
PROSITE; PS00025; P_TREFOIL; 6.
PROSITE; PROBIDIAN SKIN; Glycoprotein; Alternative splicing.
NON TER 1 144 8 X 8 AA APPROXIMATE TANDEM REI P-TYPE TISSUE-Skin; MEDLINE-93077556; Pubmed-1447205; 3-4. 3-5. 3-7. 3-8. 3-9. 8 EMBL; L02115; AAA74725.1; -. PIR; A45155; A45155. 4119 4119 4119 4431 4453 472 472 479 479 479 515 Xenopus FROM N.A. NCBI_TaxID=8355; 402 412 420 420 444 454 461 473 492 492 Xenopodinae: SEQUENCE REPEAT REPEAT REPEAT REPEAT REPEAT DOMAIN REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT DOMAIN REPEAT REPEAT REPEAT DOMAIN REPEAT

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48; Mismatches 276;
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-: SUBCELLULAR LOCATION: NUCLEAR.
-: PTM: THE TANDEM 7 RESIDIES REPEATS CAN BE HIGHLY PHOSPHORYLATED.
THE PHOSPHORYLATION ACTIVATES POLS.
-: MISCELLANEOUS: THREE DISTUNCY ZINC-CONTAINING RNA POLYMERASES ARE FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE II FOR THE MRNA PRECURSOR, AND TRNA GENES.
-: SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
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                     463
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01-MAR-1992 (Rel. 21, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-NOV-1988 (Rel. 21, Last Sequence update)
01-NOV-1992 (Rel. 21, Last Sequence update)
02-AUG-2001 (Rel. 40, Last annotation update)
03-AUG-2001 (Rel. 40, Last annotation update)
04-DIRECTED RAP POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPBI).
MUS musculus (Mouse).
05-MUS (Mouse).
05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181; Conservative 101; Mismatches 167; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.1%; Score 503.5; DB 1
33.3%; Pred. No. 5.5e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1970 AA.
       IPR000684; RNA_polII_repeat.
                                        IPR00722; RNA_pol_A.
IPR002879; RNA_pol_A2.
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P08775;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
MEDLINE-87280135; PubMed-3038894;
MEDLINE-87280135; PubMed-3038894;
Ahearn J.M. Jr., Bartolomei M.S., West M.L., Cisek L.J., Corden J.L.;
"Cloning and sequence analysis of the mouse genomic locus encoding the largest subunit of RNA polymerase II.";
J. Biol. Chem. 262:10695-10705(1987).
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SUBGNIT: RNA POLYMERASE II CONSISTS OF 12 DIFFERENT SUBGNITS.

SUBGRILLULAR LOCATION: NUCLEAR.

PTW: THE TANDEM 7 RESIDUES REPEATS CAN BE HIGHLY PHOSPHORYLATED.

THE PHOSPHORYLATION ACTIVATES POL2.

MISCELLANEOUS: TRRE DISTINCT ZING-CONTAINING RNA POLYMERASES ARE FOUND IN BURARYCTIC NUCLEI: POLYMERASE I FOR THE RIBOSCHAL RNA PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE III FOR THE MRNA PRECURSOR, AND POLYMERASE III FOR SAND TRNA GENES.

SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1567 PTPGSPGSPGPSSPYIPSPGGAMSPSYSPTSPA-YEPRSPGGYTPQSPSYSPTSPSY-SP 1624
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| R | RRBL; M14101; AA440071.1; JOINED. |
| PIR; A28490. A28490. |
| RIC: 98066; RRQ-1. |
| InterPro; IPR000684; RNA_POL_A. |
| InterPro; IPR002879; RNA_POL_A. |
| R | InterPro; IPR002879; RNA_POL_A. |
| R | ROSTEP; PS00115; RNA_POL_A.; I. |
| PROSTEP; PS00115; RNA_POL_A.; I. |
| R | ROSTEP; PS00115; RNA_POL_A.; I. |
| PROSTEP; PS00115; RNA_POL_I.REPEAT; 42. |
| R | ROSTEP; ROSTEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                257 PIPTIPKEPASTIPKE-PIPTIIKSAPIIPKEPAPTITKSAPTIPKE-----PAPTITKE 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corden J.L., Cadena D.L., Ahearn J.M. Jr., Dahmus "A unique structure at the carboxyl terminus of th of eukaryotic RNA polymerase II ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of eukaryotic RNA polymerase II.;
Proc. Natl. Acad. Sci. U.S.A. 82:7934-7938(1985)
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llarity 33.1%; Pred. No. 8.7e-14;
Conservative 101; Mismatches 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REVISIONS, AND PRESENCE OF AN ADDITIONAL EXON.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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TIPKEPAPITKEPAPITPKEPAPIAPKKPAPTTPKEPAPITPKEPAPITIKEPSPITPKE 428
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MEDLINE-88309990; PubMed=2457365;
Dautigny A., Pham-Dinh D., Roussel C., Felix J.M., Nussbaum J.L.,
Jolles P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPT-STTSDK
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01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 40, Last annotation update)
20-AGG-2001 (Rel. 40, Last annotation update)
NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN)
(NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H) (FRAGMENT).
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MEDLINE=89065087; PubMed=3143606;
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SEQUENCE OF 318-831 FROM N.A.
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P16884; Q63368;
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RX MEDLINE-89184647; PubMed=2928342;
RA Lieberburg I., Spinner N., Snyder S., Anderson J., Goldgaber D.,
RA Smulowitz M., Carroll Z., Emanuel B.S., Breither J., Rubin L.;
RT "Cloning of a cDNA encoding the rat high molecular weight
RT reloning of a cDNA encoding the rat high molecular weight
RT record in applied of its human homologue to chromosomes 1 and
RT 22.";
RT HE rat, and mapping of its human homologue to chromosomes 1 and
RT 22.";
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CC -1 - FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROFEINS: L, M,
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Pred. No. 5e-14;
); Mismatches 307; Indels 146;
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L -> T (IN REF. 2).
L -> T (IN REF. 2).
M -> T (IN REF. 2).
A -> V (IN REF. 1).
A -> V (IN REF. 1).
C -> E (IN REF. 1 AND 4).
C -> E (IN REF. 2 AND 4).
P -> S (IN REF. 2 AND 4).
P -> T (IN REF. 2 AND 4).
P -> T (IN REF. 2 AND 4).
P -> T (IN REF. 2 AND 4).
A -> V (IN REF. 4).
A -> V (IN REF. 4).
A -> C (IN REF. 4).
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R -> P (IN REF. 2 AND 4).
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AA8 7064 1 MAWKTLPIYLLLLLSVFVIQ.....ARAITTRSGQTLSKVWINCP 1311 Perfect score: Sednence: Title:

BLOSUM62

Scoring table:

Total number of hits satisfying chosen parameters:

212252 segs, 22503292 residues Gapop 10.0 , Gapext 0.5 Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

/cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/RDCOMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:* Issued_Patents_AA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RIES	Description	3-429A-4 Sequence 4. Appli	Segmence	Dated NO	Segmence 3	Sequence 5,	9	Sequence 2,	18-2 Sequence 2	Δ,	9-5 Sequence 5	-5 Seguence 5.	Sequence 5,		Sequence 2.	Segmence 2.	Sequence 23,	2 Sequence	3 Sequence 53,	Sequence	03 Sequence 103,	1 Sequence 101,	Sequence 75, A	Sequence 103		Sequence 2, 1	9 Sequence	10 11 11 11 11 11
SUMMARIES	OI .	US-09-103-429A-		5202236-25		_		US-07-638-431-2	PCT-US92-	5202236-13	US-09-219-849	US-08-479-537A	US-09-083-116-5	US-08-479-537A-2	US-09-083	US-08-276	US-09-041	US-08-642-255-13	US-08-397	0S-08	0S-08	0S-08	0S-08	ns-08	0S-08	0S-08		
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de	Query	7.4	7.2	7.2	7.1	6.9	6 9	6.9	6.9	6.7	6.4	6.0	9.0	9.0	9	5.9	5.9	5.9	5.9	5.9	5.9	5.9	5.9	5.9	5.9	5.9	0. 0.	
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7.4%; Score 522; DB 4; Length 805; 27.8%; Pred. No. 1.5e-25;

Query Match Best Local Similarity

65, Appl 65, Appl 126, App	36, Appli	1, Appli 2, Appli 34, Appl	114, App 26, Appl 52, Appl	120, App 31, Appl 28, Appl	28, Appl 28, Appl
Sequence (Sequence (Sequence)	Sequence Sequence (Sequence (Sequence Sequence Sequence		Sequence	Sequence
US-08-475-411A-65 US-08-478-029A-65 US-08-642-255-126	US-08-397-633A-36 US-08-296-791-6 PCT-US95-10661A-6	US-08-904-263A-4 US-08-325-267A-2 US-08-707-237A-84	US-08-642-255-114 US-08-397-633A-26 US-08-642-255-62	US-08-642-255-120 US-08-397-633A-31 US-08-320-559-28	US-08-545-860D-28 PCT-US94-04496-28
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ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Granados, Robert R
APPLICANT: Wang, Ping
TITLE OF INVENTION: A No. 6187558el Invertebrate Intestinal Mucin
TITLE OF INVENTION: CDNA and Related Products and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Pinnisi & Michaels, P.C.
STREET: 118 No. 6187558th Tioga
                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 14850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
OMERATING SYSTEM: DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/99/103,429A
FILING DATE: 24-JUN-1998
CLASSIFICATION NUMBER: B1.390
ATTENEY/AGENT INFORMATION:
NAME: Michaels, Christopher A
REGISTRATION NUMBER: B1.39
FELECOMMUNICATION NUMBER: B1.39
TELECOMMUNICATION NUMBER: B1.39
TELECOMMUNICATION NUMBER: B1.39
TELECOMMUNICATION NUMBER: B1.39
TELECOMMUNICATION NUMBER: B1.39
TELEFAX: (607) 256-2000
TELEFAX: (607) 256-300
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                     Sequence 4, Application US/09103429A Patent No. 6187558
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STRANDEDNESS: sir
TOPOLOGY: linear
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US-09-103-429A-4
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ANTI-SENSE: N
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US-09-103-429A-4
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TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-928-361B-5
                                                                                          COMPUTER READABLE FORM:
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  Palo Alto
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                                               USA
                                                                                                                  MEDIUM TYPE:
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Best Local Simil
Matches 295;
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  Gaps
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    342;
    Indels
                                                  TSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAP-
211;
    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELSAEPTPKALENSPKEPGVPTTKTPAATKPE 817
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US-08-9283-161B-5
US-
    33;
    Conservative
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ADDRESSEE: PETERS, VI
STREET: 385 Sherman
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547 AKGATYVGVIGKDGRIENGMAFTMIPNDDTHVRFRFKVKDVGNTISVRCGKGAGKLEFPD 606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---APTTPKEPAPTT---PKEPAPTTTKEPS-PTTPKEPAPTTTKS- 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 KVTTPDTSTTQHNKVSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETTVETKETTT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TNKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PITPKEPASTIPKEPIPITIKSAPITPKEP--APITIKSAPITPKEPAPITKEPAPITP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --TAPKEPAP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AKYGAIHSGYQTSADFVTTTTAKPTTTTGAPGQPTTTTTGSPSKPTTTTTKATTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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COMPUTER: IBM PC_COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 508; DB 3; I
Pred. No. 3.1e-24;
0; Mismatches 494;
                                                                                                                                                                                                                                                             NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
TELEPHONE: 650-324-1678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---- PTPTT---
                                                                                           US/08/928,361B
                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative 100;
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                                                                                                                  12-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1837 amino acids
                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
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KKL 531 KNL 901	545 SES 961	aaa 580 Aa 1021		KGT 664			PEL 787 : 0Q0 1316	KM 844 : 1375	- 903 S 141	6 4	100	104	AF 1072 PI 1636) 	
GQIADTSNLFPVQTHKSTGLPIDPMVGLPFDPKSGNLVHPYTNQTMSGLSVSYLAA	T	KPAPTTPEELAPTTPEEPTPTTPEEPAPTTPKAAA 	PNTPKEPAPTTPKEPAPTTPKE	PTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTKEPTSTTSDKPAPTTPKGT 	APTT PKEPAPTTPKGTAPTTLKEPAPTTPKKPAPK	ELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKETAPTTPKEPA DENGNLFDPSTKLPIDGNNQLVNPETNSTVSGSTSGSTKPKPGIPVNGGSVVPDEEAKDQ	PTTEKKPAPTTPETPPPTTSEVSTPTTKE-PTTIHKSPDESTPEL ADKGKDGLIVPPTNSINKDPVINIQYSNTTGNIINPETGKVIPGSLPGSLNYPSFNTPQQ	SAEPTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKM :	TKETATTTEKTTESKITATTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTT 	IMNKPEETAKPKDRATNSKATTPKPQKP-TKAPKKPTSTKKPKTMPRVRKPKT 	TPTPRKMISIMPELNPISKIAEAMLQTTTRPNQTPNSKLVEVNPK-SEDA	GGAEGETPHMLLRPHVEMPEVTPDMDYLPRVPNQCIII	NPMLSD	RGHYF 1077 1 1 SGKYF 1641	ESULT 3 202236-25 202236 ESULT 0. 5202236 EAPLICANT: MAUGH, KATHY J.:ANDERSON, DAVID M.;STRAUSBERG, SUSAN L.:MCCANDLISS, RUSS;WEI, TENA,FILPULA, DAVID TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE NUMBER OF SEQUENCES: 39 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/528,762 FILING DATE: 25-MAY-1990 APPLICATION NUMBER: 82,456
518 - 842 A	532 T 1 902 T	546 - 962 L	581 P		665 A 1137 K	708 - 1197 D	743 -	788 S. 1317 TT	845 T	904 -	956 TI 1466 MI	1005 - 1519 NB	1043 NE : 1577 DE	1073 RG 1637 SG	BESULT 3 220236-25 220236-25 SUSAN L.; MC TITLE C PROTEIN NUMBER CURRENY APPLI
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157 PKITTAKPINPRPSLPPNSDTSKETSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKE 216
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                                                                                                                                                                                                                                                                                                                                                                             382 -APTTPKEPA--PTAPKKPA--PTTPKEPA--PTTPKEPA--PTTKEPS--PTTPKEPA 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               639 ELAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPA-
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                                                                                                                                                       Indels 175;
                                                                                                                               Length 744;
                                                                                                                         7.2%; Score 506.5; DB 6;
ilarity 29.9%; Pred. No. 1.3e-24;
Conservative 78; Mismatches 308;
FILING DATE: 07-AUG-1987
APPLICATION NUMBER: 933,945
FILING DATE: 24-NOV-1986
APPLICATION NUMBER: 60,128
FILING DATE: 13-SEP-1984
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                                                                                                                         Query Match
Best Local Similarity
Matches 239; Conserv
                                                                        ; LENGTH: 744
5202236-25
                                                              ;SEQ ID NO:25
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RESULT 4 US-09-103-429A-3

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336 РТТРКЕРАРТТРККРАРТТРКЕРАРТТРКЕРТРТТРКЕРАРТТКЕРАРТТРКЕРАРТАРК 395
                                                                                                                                                                                                                                                                                                                                723 DKPAPTTPKETAPTTPKEPAPTTPKKP 749
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/08700651B Patent No. 6015882
                                                                                                                                                                                                                                                                                                                                                             678 ---APATTPEDDDIDP--PLPNDPINP
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Best Local Similarity 22.1%
Matches 284; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----PITIKEPSPITPK- 427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238 PTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTTKSAPTTPKEPAPTTKSAP 297
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                                                APPLICANT: Granados, Robert R
APPLICANT: Wang, Ping
TITLE OF INVENTION: A No. 6187558el Invertebrate Intestinal Mucin
TITLE OF INVENTION: CDNA and Related Products and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAPTTPKEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAPTT-PKEPA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 786;
                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 24-JUN-1998
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.1%; Score 498.5; DB 4; Best Local Similarity 29.1%; Pred. No. 4.6e-24; Matches 200; Conservative 25; Mismatches 207;
                                                                                                                                            ADDRESSEE: Brown, Pinnisi & Michaels, P.C. STREET: 118 No. 6187558th Tioga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , ORGANISM: Trichoplusia ni
;
US-09-103-429A-3
                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Michaels, Christopher A
REGISTRATION NUMBER: 34,390
REFERENCE/DOCKET NUMBER: BTI-39
TELECOMMUNICATION INFORMATION:
TELEPHONE: (607) 256-2000
TELEPAX: (607) 256-368
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 786 amino acids
Sequence 3, Application US/09103429A Patent No. 6187558 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                                                                             Ithaca
                                                                                                                                                                                                                           14850
                                                                                                                                                                                                               COUNTRY:
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GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLYN
APPLICANT: LEECH, JAMES EN, CAROLYN
APPLICANT: LEECH, JAMES BY, CAROLYN
APPLICANT: LEECH, JAMES BY, C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS
TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF CRYPTOSPORTIGIUM PARVUM
TITLE OF INVENTION: INECTIONS
FILE REFERENCE: 480:19-4(HV)
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT FILING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: 08/415,751
EARLIER FILING DATE: 1999-04-03
NUMBER OF SEQ ID NOS: 15 41; 111 KKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRPS 170 171 LPPNSDTSKE-----TSLTVNKETTVETKETTTNKQTSTDGKEKTTSAK 215 ETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTP 275 276 TIIKSAPTTPKEPAPTTTKSAPTTPKEPAPTTTKEPAPTTPKEPAPTTTKEPAPTTTKSA 335 480 544 587 662 633 TAAPIT-AAPAPNITVIVPPTAAPIAAPIVAH-------APNITAAPVITIS 677 421 ADFSIDHLLPHESDCGQYLQCVHGQTIARPCPGNLHFSPATQSCESPVTAGCQVFECDSD ---PKEPAPTTPKEPAPTTKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTP EKPAPTTPEELAPTTPEEPTPTPEEPAPTTPKAAAPNT -- PKEPAPTTPKEPAPTTPKE PAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPK AAPTAAPTTAVPEIPTTVTSPPTAAPTTAAP---APNTT------VTVPP GTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTS 6.9%; Score 489; DB 3; Length 1721; 22.1%; Pred. No. 4.5e-23; ative 82; Mismatches 476; Indels 44: 159 APCNSENSFEQGQIFDMGSKVYIPYTKCVGVKHTTTTTTTTTTTTTTTT --APTTPKKPAPTT

RESULT

, Carolyn PEPTIDES, GLYCOPROTEINS, THEIR EUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM SPECIES INFECTIONS 41; 240 336 РТТРКЕРАРТТРККРАРТТРКЕРАРТТРКЕРТРТТРКЕРАРТТКЕРАРТТРКЕРАРТАРК 395 111 KKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRPS 170 171 LPPNSDTSKE-----TSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAK 216 ETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTP **TTIKSAPTTPKEPAPTTTKSAPTTPKEPAPTTTKEPAPTTPKEPAPTTKEPAPTTTKSA** 159 APCNSENSFEQGQIFDMGSKVYIPYTKCVGVKHTTTTTTTTTTTTTTTTTT------**KPAPTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTT** Indels 442; 116 RSNETK---TTEPSANTYAGVYRSN-ETKTTEPSANT---NFLLVDPKI-----Length 1721; OPERATING SYSTEM: PC_DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: 6.9%; Score 489; DB 3; 22.1%; Pred. No. 4.5e-23; tive 82; Mismatches 476 480.76-1(HV) омыек: US/08/928,361B 12-SEP-1997 3: PETERS, VERNY, JONES & 385 Sherman Avenue, Suite us 60/026,062 US/08928361B NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480
TELECOMMUNICATION:
TELEPHONE: 650-324-1677 IBM PC compatible 9 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 66
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION: COUNTRY: USA
ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk 1721 amino acids Best Local Similarity 22.19 Matches 284; Conservative TELEFAX: 650-324-1678 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: TOPOLOGY: linear MOLECULE TYPE: protein US-08-928-3618-6 APPLICANT: Petersen, C TITLE OF INVENTION: PH TITLE OF INVENTION: TF TITLE OF INVENTION: FF TITLE OF INVENTION: SI NUMBER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS: APPLICATION NUMBER: Sequence 6, Application Patent No. 6071518 STREET: 30. amino acid Patent No. 6071518 GENERAL INFORMATION: APPLICANT: Peterse CLASSIFICATION: FILING DATE: STRANDEDNESS ADDRESSEE: COMPUTER: Query Match 209 276 241 301 351 g g 셤 셤 g ð Q ŏ g à à

APPLICANT: Rogers IV, William O. TITLE OF INVENTION: Protective malaria sporozoite surface protein IIILE OF INVENTION: immunogen and gene CORRESPONDENCE ADDRESS:
ADDRESSEE: A David Spevack
STREET: NMRDC Building 1 T-12 National Naval
STREET: Medical Center COUNTRY: USA
ZIP: 20814-5044
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/638,431
FILLING DATE: 19910110 CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SPEVACK, AVYON D.
TELECOMMUNICATION INFORMATION:
TELEFAN: (301) 295-6759
TELEFAN: (301) 295-6759
INFORMATION FOR SEQ ID NO: 2: Richard Srisin : 826 amino acids AMINO ACID SEQUENCE CHARACTERISTICS: , MOLECULE TYPE: protein US-07-638-431-2 Hedstrom, F Khusmith, S NUMBER OF SEQUENCES: linear CITY: Bethesda STATE: MD TOPOLOGY:

34; PKEPI------NPEESNPKEP----INPEDNENPLIIQDEPIEPRNDSNVIPI 649 274 TPTTIKSAPTTPKEPA-PTTTKSAPTTPKEPA-PTTTKEP----APTTPKEP-APTTKE 326 327 РАРТТТКЅАРТТРКЕР-АРТТРККР-АРТТРКЕР-АРТТРКЕР-ТРТТРКЕРАРТТКЕРА 382 383 PITPKEPAPIAPK--KPAPITPKEPAPITPKEPAPITIKEPSPITPKEPAPITIKSAPIT 440 441 TKEPAPTTTKSAPTTPKEPSPTTTKEPAPTTPKEPA-PTTPKKP-APTTPKEPAPTTPKE 498 TIPEEPTPTTPEEPAPTTPKAAAPNTPKEP-APTTPKEPAPTTPKEPAPTTPKETAPTTP 616 PAPTTTKKPAPTAPKEP-APTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAP 557 KGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTT PKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPT Indels 149; Length 826; Query Match
6.9%; Score 488.5; DB 1;
Best Local Similarity 26.4%; Pred. No. 2.1e-23;
Matches 153; Conservative 54; Mismatches 223; 193 558 219 524 QQ ò QΫ́ 셤 Ωy Db Q g Ω g Ω g

2y 73 Db 68 Qy 75	737 TPKEPAPTTPKKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAE 790
RESULT B PCT-US92-06 CGENERAL APPLICA APPLICA APPLICA APPLICA APPLICA ADDE STRE STRE STRE STRE STRE STRE STRE STR	PERSULT 8 PCT-US92-00018-2 Sequence 2, Application PC/TUS9200018 Sequence 2, Application PC/TUS9200018 APPLICANT: Charcenvitt Yulin APPLICANT: Charcenvitt Yulin APPLICANT: Charcenvitt Yulin APPLICANT: Rogers IV William O. TITLE OF INVENTION: Protective malaria sporozoite surface protein TITLE OF INVENTION: Protective malaria sporozoite surface protein TITLE OF INVENTION: Protective malaria sporozoite surface protein TITLE OF INVENTION: Immunogen and gene encoding APPLICANT: Rogers IV William O. TITLE OF INVENTION: Immunogen and gene encoding CORRESPONDENCE ADDRESS: ADDRESSE: A Darid Spewack STREET: MARC Building I T-12 National Naval STREET: MARC Building I T-12 National Naval STATE: MAGC Building I T-12 National Naval STATE: MAGC Building I T-12 National Naval CORRESPONDENCE COMPATION COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: Propey disk COMPUTER: Propey disk COMPUTER: READABLE FORM: MEDIUM TYPE: Propey disk COMPUTER: 1920103 ATTORNAME: ASSTER: PC-DOS/WS-DOS CORRESPT APPLICATION NUMBER: PC-DOS/WS-DOS CORRESPT APPLICATION NUMBER: PC-DOS/WS-DOS CORRESPT APPLICATION NUMBER: PC-DOS/WS-DOS COMPUTER: NUMBER: PC-DOS/WS-DOS COMPUTER: NUMBER: PC-DOS/WS-DOS COMPUTER: ATTORNAME (301) 295-6759 TELEPHONE: (301) 295-6759 TELEPHONE: (301) 295-6759 TYPE: AMINO ACID
Query Me Best Loc Matches Qy 274 Db 273	Query Match 6.9%; Score 488.5; DB 5; Length 826; Best Local Similarity 26.4%; Pred. No. 2.1e-23; Matches 153; Conservative 54; Mismatches 223; Indels 149; Gaps 34; 274 TPTIKSAPTTPKEPA-PTTTKSAPTTPKEPA-PTTTKEPAPTTPKEP-APTTKE 326 1
97 37 36 97 37 98 98 98 98 98 98 98 98 98 98 98 98 98	327 PAPTITKSAPITPKEP-APTIPKKP-APTIPKEP-TPTIPKEPATITKEPA 382

45; 196 -----PSNPEEPNPEE--PSNPKEP----SNPEEPINPEELNPKEPSNPEESN 606 737 TPKEP-----APTTPKKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAE 790 217 TOSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKE----PASTTPKE 272 273 PTPTTIKSAPT-TPKEPAPTTTKSAPTTPKEPAPTTTKEPAPTTTPKEPAPTTTKEPA--P 329 385 TPKEPAPTAPKKPA--PTTPKEPA--PTTPKEPAPTTTKEPSPTTP-----KEPAPTTTK 435 SAPITIKEPA-----PITIKSAPITPKEPSPITIKEPA--PITPKEPA----PITPKK 482 253 AKPTYKAKPTYKAKPTYPSTYKAKPTYP----PTYKAKPSYPPTYKAKPTYKAK 308 157 PKITTAKPINPRPSLPPNSDTSKETSLTVNKETTVETKETTTNKQTSTDGKEKTTSAKE 216 40 558 TTPEEPTPTTPEEPAPTTPKAAAPNTPKEP-APTTPKEPAPTTPKEPAPTTPKETAPTTP PKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPT 80 SYPPIYKSKPITYPPIYKAKPSYPPIYKPKKIYPPI-YKPKITYPPIYKPKASYP 330 ТТТКЅАРТТРКЕРАРТТРККРАРТ-ТРКЕРАРТТ----РКЕРТРТРКЕРАРТТКЕРАРТ 617 KGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTT 11 PKMTYPPTYKPKPSYPP------TYKSKPTY------KPKIT----524 SNPNE--PLNPNEP------SNPNEPSNPNEPSNPEE--PSNPKE--PSNPNE----Indels 169; Length 652; APPLICANT: MAUGH, KATHY J.; ANDERSON, DAVID M.; STRAUSBERG, SUSAN L.; MCCANDLISS, RUSS; WEI, TENA; FILPULA, DAVID ; TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE 6.7%; Score 476.5; DB 6; 29.7%; Pred. No. 9.2e-23; ative 71; Mismatches 284; 707 PYKGHEERIPKPHRSNDDYVYDNNVNKNNKDEPEIPNNE 745 791 PTPKALENSPK-------EPGVPTTK 809 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-MAY-1990
AIDLING DATE: 07-AUG-1987
APPLICATION NUMBER: 833,945
FILING DATE: 24-NOV-1986
APPLICATION NUMBER: 650,128
FILING DATE: 13-SEP-1984 Conservative SEQUENCES: 39 Query Match Best Local Similarity Matches 221; Conserv ; Patent No. 5202236 ; LENGTH: 652 5202236-13 NUMBER OF ID NO:13: -- ès RESULT 9 5202236-13 677 493 565 41 ; PROTEIN à g ò g οÿ g δý g οy d á Op ò g δ g ò g ŏ g

Qy 352 PTT	 Db 187 P	оу 391	Db 245 PAG	Qy 437 API	299	494	24. r	Qy 544 PEK Db 405 SRI	599	Db 463 GAF	Qy 642 PT1	Db 523 PPC	Oy 697 API	Db 581 GP-	Oy 749 PAI	Db 637 PG	Фу 800 РК	:: Db 696 SRI	RESULT 11 US-08-479-537 ; Sequence 5,	; Fatent No.; GENERAL IN	; APPLICAN ; APPLICAN	; APPLICAN ; TITLE OF	; TITLE OF ; NUMBER (; COKKESPO ; ADDRES : STREET	STATE:	; ZIP: ; COMPUTEI ; MEDIUN	; COMPUT ; OPERAT ; SOFTW	CURRENT APPLIC FILING	CLASSI PRIOR AN PAPPLIC FILINC
NO -	TAPKEPAPTTPKETAPTTPKKLTPTTPEK 538	YCHANFSIFFIINVNFI YUUNAKE KAMAMMA KAMAMA KAMAMMA KAMAMA KAMAMMA KAMAMMA KAMAMMA KAMAMMA KAMAMMA KAMAMMA KAMAMMA KAMAMA KAMAMA KAMAMMA KAMAMA KAMAMAMA KAMAMA			FOR THE PRESENT TO THE TOTAL TO THE PROPERTY TO THE DEPT. THE PROPERTY TO THE DEPT. THE PROPERTY TO THE DEPT. THE DE	TPKGTAPTILKEPAPTTPKKP 704	: : YPPTYRAKPSYPPTYRAKP 521	0.y TTPKEPA - PTTFPETP 757 DS : : DD	PTYKAKPSYPPTYKAKPTYPSTYKAKPSYP 576 '	AEPTPKALENSFKEPGVPTTKTPAATKPE 817	KPIIPSIINANFS	qa	QY	qQ · ·	QY	qq	O	qa .		APPLICATION AND ALSO THE	849				ificial Sequence: Illustrative	52; DB 4; Length 960;	d. No. 5.1e-21; Mismatches 309; Indels 134; Gaps 41;	TPKEPTPTTIKSAPTTPKEPAPTTTKS 295	
	483	א מי	() 539 LAFTTPEKPAPTTPEELAFTTPEEPTPITPEERA-PITPKAAARNIPKEEPTTFN 1	101111111111111111111111111111111111111	OY 394 EPA-FILTFREPARTIFERETITT FROMERTILABERATITER FREE BETATION TO THE FORMER FREE BETATION TO THE FORMER FREE BETATION TO THE FREE	647	Db 474 KPIYPSIYKAKPIYKAKPSYPPIYKAKPS	OY 705 APKELAPTITKGPTSTTSDKPAPTIPKETAPTTPKEPAPTTPKKPA-PIT	- Δ-	758 PPTTSEVSTPTTTKEPT	O// PIIKANPSIPPIIKAKPSI	OY 010 MITTARONITEROLETIFETITAMP 042 DD 621 YPPTHKAKTYKAKSYPPTHKAKP 645		RESULT 10	Sequence 5, Application US/09219849	GENERAL INFORMATION:		; APPLICANT: BOUWSTRA, JAN B. ; APPLICANT: DE WOLF, FREDERIK A. ; APPLICANT: MOOBROEK, ANDREAS	WERTEN, N WIND, RIC VAN DEN I	; TITLE OF INVENTION: SULTABLE FOR PHOTO TITLE OF INVENTION: PREPARATION THEREO	CURRENT APPLICATION NUMBER: US/09/219,849 CURRENT FILING DATE: 1998-12-23	; NUMBER OF SEQ ID NOS: 50 ; SOFTWARE: Patentin Ver. 2.1	; SEQ ID NO 5 ; LENGTH: 960	; TYPE: PKT ; ORGANISM: Artificial Sequence : FRATHIRE:	; OTHER INFORMATION: Description of Artificial Sequence: Illustrative; OTHER INFORMATION: amino acid sequence US-09-219-849-5	Query Match	Best Local Similarity 25.6%; Pred. No Matches 173; Conservative 60; Misma	QY 238 PTPKAETTTKGPALTTPKEPASTTPKEPASTTPKEPASTTTKSAPTTPKEPAPTTTKS	QY 296 APTTPKEPAPTTTKEPA-PTTPKEPAPTTTKEPAPTTTKSAPTTPKEPAPTTPKKPA

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-----PTAPK-KPAPTTP---KEPAPTTPKEPA-PTTTKEPSPTTPKEPAPTTKS 436
                                                                                                                                PGSRDPGP-----PGAPGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGP 348
                                                                                                                                                                                                                                                                                                                                      KEPA-----PITPKET-APITPKGT-----APITLKEPAPITPKKP-APKELA 641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIKEPISITSDKPAPIIPKGIA-PITPKEPAPITP---KEPAPIIPKGIA-PITLKEP 696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -PGAPGPAGPPGSRDPGPPGAPGPAGPPGSRDPGPPGAHGPAGPKGAHG 244
                                                                                                                                                                                                   PITIKEPAPITIKSAPITPKEPSPITIKEPAPITPKEPAPITP---KKPAPITPKEPAP 493
                                                                                                                                                                                                                                                                                                  P---KEPAPTTKKPA-----PTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTT 543
                                                                                                                                                                                                                                                                                                                                                                                                  KPAPT-TPEELAPTTPEEPTPTTPEEPAPTTPKAAA-PNTPKEPAPTTP---KEPAPT 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTTP----ETPPPTTSEVSTPTTTKEPTTHKSPDESTPELSAEPTPKALEN----S 799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANT: CHAMBON, Pierre
ANT: KIENY, MATIE-Paule
ANT: LATHE, RICHARD
ANT: LATHE, RICHARD
ANT: HARBUVENI, MARA
OF INVENTION: PHARMACEUTICAL COMPOSITION FOR THE
OF INVENTION: TREATMENT OR PREVENTION OF A MALIGNANT TUMOR
OF SEQUENCES: 5
PONDENCE ADDRESS:
ESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
ESSEE: BURNS, DOANE, SALAGA
TPKEPAPTTP---KEPTPTTPKEPA--PTTKEPAPTTPKEPA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ER READABLE FORM:
UM TYPE: Floppy disk
UTER: IBM PC compatible
ATING SYSTEM: PC-DOS/MS-DOS
WARE: Patentin Release #1.0, Version #1.30
I APPLICATION DATE: US/08/479,537A
NG DATE: 07-UN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIFICATION: 514
APPLICATION DATA:
JCATLON NUMBER: FR 90/13101
APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5, Application US/08479537A . 5861381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRY: Virginia
PRY: United States
22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPGVPTTKTPAATK 815
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990 -PNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIINPMLSD 1048
                                                                                            241 APDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS 300
                                                                                                                                                                                   301 APDXRP-XPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                 575 TPKA----AAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGT-APTTLKEPAP 629
181 APDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      821 APDXRPXPG----STAPXAHGVT----SAPDXRPXPGSTAPXAHGVTSAPDXRPXP- 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          930 KPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPNQT 989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1049 ETNICNGKPVDGLTT-LRNGTLVAFRGHYFWMLSPFSPPSPARRITEVWGIPSPID 1103
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                                                                                                                                                                                                                                    467 PAPTIPKEPAPTIPK----KPAPTIPKEPAPTIPK----EPAPTITKKPAPTAPKEPAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             630 TTP-----KKPAPKELAPTITKEPTSTTSDKPAP--TTPKGTAPTTPKEPAPTTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            678 KEPAPITPKG----TAPTILKEPAPITP------KKPAPKELAPITTKGPTSTTSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             814 -TKPEMTTTAKDK---TTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              870 TITQDITPFKITILKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRAINSKATTPKPQ
                                            371 PKE--PAPTTKEP-----APTTPKEPAPTAPK----KPAPTTPKEPAPTTPKEPAPTT
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                                                                                                                                                                                                                                                                                    360 SAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 472 APXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRP-XPGSTAPXAHGVTSAPDXRPXPGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      586 PXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAP-XAHGVTSAPDX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        724 KPAP--TTPK----ETAPTTPKEPAPTTP------KKPAPTTPETPPPTTSEVSTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     869 -GSTAPXAHGVTSAPDXRP--XPGSTAPXAHGVTSA-PDXRPX--------PGST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FOR THE A MALIGNANT TUMOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    768 TITKEPTT-----IHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAA----
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TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR
TITLE OF INVENTION: TREATMENT OR PREVENTION OF A MA
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
US-09-083-116-5
; Sequence 5, Application US/09083116
; Patent No. 6203795
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APPLICANT: CHAMBON, Pierre
APPLICANT: KIENY, Marie-Paule
APPLICANT: LATHE, Richard
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.xed. The number of such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Amino acid 144 is Y = Xaa
which is the codon for Thr or Asn wherein Thr = ACT, ACC,
or ACG; and Asn = AAT or AAC."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Amino acid 147 is X2 = Xaa
which is the codon for Pro or Ala wherein Pro = CCT, CCC,
or CCG; and Ala = GCT, GCC, GCA, or GCG."
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which is the codon for Pro or Ala wherein Pro = CCT,
or CCG; and Ala = GCT, GCC, GCA, or GCG."
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23.7%; Pred. No. 6e-19;
-ive 69; Mismatches 511; Indels 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "The amino acids spanning
128 to 1727 constitute a repeated regio
20 amino acids, 17 of which are fixed.
repeats varies from 1 to 40."
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                                                                                                                                                                                          ATJOURDE, TESKIN, ROBIN L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 017753-025
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1867 amino acids
       FILING DATE: 23-60T-1991
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,320
FILING DATE: 04-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/403,576
FILING DATE: 14-WAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 23.7%
Matches 255; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
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LOCATION: 128..1727
OTHER INFORMATION: //
OTHER INFORMATION: 2/
OTHER INFORMATION: 2/
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MOLECULE TYPE: peptide
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LOCATION: 147
O'THER INFORMATION:
O'THER INFORMATION:
'O'THER INFORMATION:
FEATURE:
NAME/KEY: Peptide
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OTHER INFORMATION:
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US-08-479-537A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  472 APXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRP-XPGSTAPXAHGVTSAPDXRPXPGS 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           930 KPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPNQT 989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  869 -GSTAPXAHGVTSAPDXRP--XPGSTAPXAHGVTSA-PDXRPX------PGST 911
                                                                                             239
                                                                                                                                                                                                                                                        TTPKEPAPTTT-----KSAPTTPKEP------APTTKEPAPTTPKEPAPTT 323
                                                                                                                                                                                                                                                                                                                                                                                                                    371 PKE--PAPTTKEP-----APTTPKEPAPTAPK----KPAPTTPKEPAPTTPKEPAPTT 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 418 TKEPSPTTPKEPAPTT--TKSAPTTTKEPAPTT----TKSAPTTPKEPSPTTK----E 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTP-----KKPAPKELAPTITKEPTSTTSDKPAP--TTPKGTAPTTPKEPAPTTP 677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  814 -TKPEMTTTAKDK---TTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTS
                                                                                                                  324 TKE--PAPTTT-----KSAPTTPKEPAPTTPK----KPAPTTPKEPAPTTPKEPTTT
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                                                                                               181 TSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKD-LAPTSKVLAKPT
                                                                                                                                                                          --TPTTPKEPASTTPKEPTPTTIKSAP
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                Length 1867;
                                                        Indels
, DB 4;
6e-19;
                                                      Mismatches
                6.0%; Score 424.5;
23.7%; Pred. No. 6e-
tive 69; Mismatches
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                                                                                                                                                                               240 P-KAETTTKGP--ALTTPKEP-
                                                            Conservative
                               Local Similarity
es 255; Conserv
                    Query Match
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128 to 1727 constitute a repeated region wherein the repeat
20 amino acids, 17 of which are fixed. The number of such
repeats varies from 1 to 40."
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which is the codon for Pro or Ala wherein Pro = CCT, CCC,
or CCG; and Ala = GCT, GCC, GCA, or GCG."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Amino acid 147 is X2 = Xaa
which is the codon for Pro or Ala wherein Pro = CCT, CCC,
or CCG; and Ala = GCT, GCC, GCA, or GCG."
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which is the codon for Thr or Asn wherein Thr
or ACG; and Asn = AAT or AAC."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Amino acids 1 to 21 are a 21 amino acid precursor sequence."
                                                                                                                                                                                                   Version #1.30
                                                                                                                                                                                                                                                                                                                                                          PRIOR PAPLICATION DATA:
APPLICATION NUMBER: W0 PCT/FR91/00835
FILING DATE: 23-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,320
FILING DATE: 04-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/403,576
                                                                                               ZIP: 22313-1404
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/083,116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE DOCKET NUMBER: 017753-025
TELECOMMUNICATION: TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Teskin, Robin L. REGISTRATION NUMBER: 35,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 14-MAR-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1867 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (703) 836-2021 INFORMATION FOR SEQ ID NO:
                                                                : Virginia
RY: United States
22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Peptide
LOCATION: 128..1727
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 144
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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144
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CTHER INFORMATION:
CTHER INFORMATION:
US-09-083-116-5
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OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
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                    : P.O. Box
Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
LOCATION:
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NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION
                                                                                 COUNTRY:
                                         CITY:
STATE:
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- ACT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      420 SAPDXRPXPGSTAPXAHGVTS----APDXRPXPGSTAPXAHGVTSAPDXRPX----PGST 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              472 APXAHGVISAPDXRPXPGSTAPXAHGVISAPDXRP-XPGSTAPXAHGVISAPDXRPXPGS 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAP 762
                             /note= "Amino acid 144 is Y = Xaa
which is the codon for Thr or Asn wherein Thr
or ACG; and Asn = AAT or AAC."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 -- DNKPAPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 APDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 APDXRP-XPGSTAPXAHGVŢSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       645 RPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGS--TAPXAHGVTSAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---TPTTPKEPASTTPKEPTPTTIKSAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTPKEPAPTTT-----KSAPTTPKEP-----APTTKEPAPTTPKEPAPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         324 TKE--PAPTIT-----KSAPTIPKEPAPTIPK----KPAPTIPKEPAPTIPKEPTPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            418 TKEPSPTTPKEPAPTT - TKSAPTTTKEPAPTT - - - - TKSAPTTPKEPSPTTK - - - E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAPTTPKEPAPTTPK ----KPAPTTPKEPAPTTPK ----EPAPTTKKPAPTAPKEPAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        630 TTP-----KKPAPKELAPTTTKEPTSTTSDKPAP--TTPKGTAPTTPKEPAPTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   531 TAPXAHGVTSAPDXRPXPGSTAP-XAHGVTSAPDXRPXPGSTAPXAHGVTS----APDXR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         371 PKE--PAPTIKEP-----APTIPKEPAPTAPK----KPAPTIPKEPAPTIPKEPAPTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  519 TPKETAP----TTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     575 TPKA----AAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGT-APTTLKEPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              678 KEPAPTTPKG----TAPTTLKEPAPTTP------KKPAPKELAPTTTKGPTSTTSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360 SAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      768 TTTKEPTT-----IHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAA-----
                                                                                                                                                        /note= "Amino acid 147 is X2 = Xaa
which is the codon for Pro or Ala wherein
or CCG; and Ala = GCT, GCC, GCA, or GCG."
                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 241;
                                                                                                                                                                                                                                                                                                                                                                                             Length 2035;
                                                                                                                                                                                                                                                                                        /note- "Amino acids 1 to 21 are a 21 amino acid precursor sequence.
                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                       69; Mismatches 511;
                                                                                                                                                                                                                                                                                                                                                                                             6.0%; Score 424.5; DB 233.7%; Pred. No. 6.6e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 724 KPAP--TTPK----ETAPTTPKEPAPTTP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-KAETTTKGP--ALTTPKEP-----
                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 23.79
Matches 255; Conservative
                                                                                                                                                                                                                                      NAME/KEY: Peptide
COCATION: 1.21
OTHER INFORMATION:
US-08-479-537A-2
        LOCATION: 144
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                         FEATURE:
NAME/KEY: Peptide
LOCATION: 147
CHER INFORMATION:
OTHER INFORMATION:
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Xaa Xaa which is the codon for Pro or Ala wherein Pro
CCC, CCA, or CCG; and Ala = GCT, GCC, GCA, or GCG."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "The amino acids spanning
128 to 1899 constitute a repeated region wherein the
20 amino acids, 17 of which are fixed. The number of
repeats varies from 1 to 40."
Sequence 2, Application US/08479537A
Patent No. 5861381
GENERAL INFORMATION:
APPLICANT: CHAMBON, Pierre
APPLICANT: LATHE, Richard
APPLICANT: LATHE, Richard
APPLICANT: HARBUVEN! Mara
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR THE
TITLE OF INVENTION: TREATMENT OR PREVENTION OF A MALIGNANT TUMOR
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P. STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 017753-025
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-5021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 90/13101
FILING DATE: 23-0CT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR91/00835
FILING DATE: 23-0CT-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/479,537A FILING DATE: 07-JUN-1995 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/039,320 FILING DATE: 04-APR-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/403,576 FILING DATE: 14-WAR-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2035 amino acids
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LOCATION: 128.1899
OTHER INFORMATION: /n
OTHER INFORMATION: 12
OTHER INFORMATION: 20
OTHER INFORMATION: 20
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TOPOLOGY: linear
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MOLECULE TYPE: peptide
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NAME/KEY: Peptide
LOCATION: 134
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
NAME/KEY: Peptide
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-PNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLSD 1048
                                                                                                                                            821 APDXRPXPG-----STAPXAHGVT-----SAPDXRPXPGSTAPXAHGVTSAPDXRPXP- 868
                                                                                                                                                                                               930 KPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPNQT 989
                                                                                                                                                                                                                                                   869 -GSTAPXAHGVTSAPDXRP--XPGSTAPXAHGVTSA-PDXRPX------PGST 911
814 -TKPEMTTTAKDK---TTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTS 869
                                              763 DXRPXPGSTAPXAHGVTSAPDXRPXPGST--APXAHGVTSAPDXRPXPGSTAPXAHGVTS 820
                                                                                               870 TTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQ 929
                                                                                                                                                                                                                                                                                                                                              ----GVTSAPDXRPXPGSTA----PXAHG 957
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   958 VTSAPDXRPXPGSTAPXAHGVTSA------PDXRPXPGSTAPXAHGVTSAPD 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: HAREUVENI, MATA
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR THE
TITLE OF INVENTION: PRATMENT OR PREVENTION OF A MALIGNANT TUMOR
NUMBER OF SEQUENCES: 5
CORRESPONDRUCE ADDRESS:
ADDRESSEE: BURNS, DONE, SWECKER & MATHIS, L.L.P.
STREET: P.O. BOX 14044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR91/00835
FILING DATE: 23-OCT-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/039,320 FILING DATE: 04-APR-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/403,576
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 08/479,537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REPERENCE/DOCKET NUMBER: 01775
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-620
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2035 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09083116
Patent No. 6203795
GENERAL INFORMATION:
GAPPLICANT: CHAMBON, Pierre
                                                                                                                                                                                                                                                                                                                                                   912 APXAHGVTSAPDXRPXPGSTAPXAH-
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LATHE, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: P.O. Box CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE
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APPLICANT:
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/note= "Amino acid 134 is X1 = Xaa Xaa Xaa which is the codon for Pro or Ala wherein Pro = CC CCC, CCA, or CCG; and Ala = GCT, GCC, GCA, or GCG."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSS
                                                                                                                                                                                                                                                                                                                                                             /note= "Amino acid 144 is Y = Xaa
which is the codon for Thr or Asn wherein Thr = ACT, ACC,
or ACG; and Asn = AAT or AAC."
                                                                                                           /note= "The amino acids spanning
128 to 1899 constitute a repeated region wherein the
20 amino acids, 17 of which are fixed. The number of
repeats varies from 1 to 40."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     = CCT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 -- DNKPAPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PKE--PAPTTKEP-----APTTPKEPAPTAPK----KPAPTTPKEPAPTTPKEPAPTT 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              418 TKEPSPTTPKEPAPTT--TKSAPTTTKEPAPTT----TKSAPTTPKEPSPTTK----E 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 APDXRP-XPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVT 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAPDXRPXPGSTAPXAHGVTS----APDXRPXPGSTAPXAHGVTSAPDXRPX----PGST 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               575 TPKA----AAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGT-APTTLKEPAP 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 TSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKD-LAPTSKVLAKPT 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TKE--PAPTTT-----KSAPTTPKEPAPTTPK----KPAPTTPKEPAPTTPKEPTFT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 APDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TPKETAP----TTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPT 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 241; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Amino acid 147 is X2 = Xaa
which is the codon for Pro or Ala wherein Pro
or CCG; and Ala = GCT, GCC, GCA, or GCG."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Amino acids 1 to 21 are a 21 amino acid precursor sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.0%; Score 424.5; DB 4;
llarity 23.7%; Pred. No. 6.6e-19;
Conservative 69; Mismatches 511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----KSAPTTPKEP-
                  TOPOLOGY: linear MOLECULE TYPE: peptide
single
                                                                       NAME/KEY: Peptide
LOCATION: 128..1899
OTHER INFORMATION: ,
                                                                                                                                                                                                        NAME/KEY: Peptide
LOCATION: 134
OTHER INFORMATION:
OTHER INFORMATION:
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CTHER INFORMATION:

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CS-09-083-116-2
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OTHER INFORMATION:
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OTHER INFORMATION:
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Best Local Similarity
Matches 255; Conserv
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STRANDEDNESS:
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LOCATION:
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A. M. Comment

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990 -PNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLSD 1048
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                                                                                                                                                                                                                                                                                                                                                                                                                                       763 DXRPXPGSTAPXAHGVTSAPDXRPXPGST -- APXAHGVTSAPDXRPXPGSTAPXAHGVTS 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                870 TTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRAINSKATTPKPQ 929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     930 KPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPNQT 989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETNICNGKPVDGLTT-LRNGTLVAFRGHYFWMLSPFSPPSPARRITEVWGIPSPID 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            912 APXAHGVTSAPDXRPXPGSTAPXAH------GVTSAPDXRPXPGSTA---PXAHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTP------KKPAPKELAPTTTKEPTSTTSDKPAP--TTPKGTAPTTPKEPAPTTP
                                                                                                 531 TAPXAHGVTSAPDXRPXPGSTAP-XAHGVTSAPDXRPXPGSTAPXAHGVTS----APDXR
                                                                                                                                             KEPAPTTPKG----TAPTTLKEPAPTTP------KKPAPKELAPTTTKGPTSTTSD
                                                                                                                                                                                 586 PXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAP-XAHGVTSAPDX
                                                                                                                                                                                                                                                                    RPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGS--TAPXAHGVTSAP
                                                                                                                                                                                                                                                                                                             768 TTTKEPTT-----IHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAA-----
                                                                                                                                                                                                                                                                                                                                                                                                814 -TKPEMTTTAKDK---TTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTS
                                                                                                                                                                                                                               KPAP--TTPK----ETAPTTPKEPAPTTP------KKPAPTTPETPPPTTSEVSTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hardy, Daniel M.
APPLICANT: Garbers, David L.
TITLE OF INVENTION: Species-Specific Egg-Binding Proteins
TITLE OF INVENTION: Sperm
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REGISTRATION NUMBER: UTSD:418\KIT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Arnold, White & Durkee STREET: P. O. Box 4433
CITY: Houston STATE: Texas
COUNTRY: USA
ZIP: 77210-4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/276,967 FILING DATE: Submitted Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
US-08-276-967-2
Sequence 2, Application US/08276967
Patent No. 5851817
CENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    713-789-2679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            614 ERTT-----TPTIRTTTPTERTT---IPTKKTT-----VPTEKTIIPT-----ERTI 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         512 PKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPEEP
                                                                                                                                                                                                                                                                                                                                              313 PSETSVSTEKPVAPTE----KPTVPSEIYTIPTEKPMVHMEKPIVHT--EKPTVPT-EKP
                                                                                                                                                                                                                                                                                                                                                                                                                          366 TIPTEKSTVPT--KKPTVFKEPTLPPE-GPTVPAE-RPTTPPEGPAVPPKG--PTVLTE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTAPTILKEPAPTTPKKPAPKELAPT-TTKGPTSTT---SDKPAPTTPKETAPTTPKEPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 743 PTTPKKPAPTTPETPPP----TTSEVSTPT----TTKEPTTHKSPDESTPELSAEPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       793 PKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         853 EKTTESKITATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETA
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                                                                                                                                                                                                                                                                                                                                                                                         572 APTTPKAAAPNTPKEPA----PTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTKEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 119;
                                                                                                                                                                                                                          Length 2476;
                                                                                                                                                                                                                                                                    43; Mismatches 177;
                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                        Query Match 5.9%; Score 419.5; DB 2
Best Local Similarity 32.5%; Pred. No. 1.7e-18;
Matches 163; Conservative 43; Mismatches 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    completed: April 26, 2002, 16:26:41
ne: 541 sec
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TELEX: 79-0944
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
TRNGTH: 2476 amino acids
                                                                  LENGTH: 2476 amino acitory TYPE: amino acidory STRANDEDNESS: single; TOPOLGGY: linear MOLECULE TYPE: protein US-08-276-967-2
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Job time:
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

April 26, 2002, 16:18:41; Search time 82.85 Seconds (without alignments) 890.006 Million cell updates/sec

US-09-556-246-1_COPY_200_1167 5155 1 VKDNKKNRTKKKPTPKPPVV.......GKPVDGLTTLRNGTLVAFRG 968 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 Total number of hits satisfying chosen parameters:

219241 seqs, 76174552 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	mucin 2 precursor		Cvst dermination s	-	extensin-like prot	nascent polypeptid	qlucan 1,4-alpha-q	high molecular mas	mucin 1 precursor.	hypothetical prote	extensin class 1 p	elastic titin - hu	hypothetical prote		nucleolar phosphop	protein UNC-89 - C	hypothetical prote			. –	Ψ	larval glue protei	hydroxyproline-ric	hypothetical prote			hydroxyproline-ric	hypothetical prote	calphotin - fruit
SUMMARIES	QI	A43932	T18262	T31108	T16251	S49915	T30826	S48478	T18535	A35175	T25697	T11622	138346	C84672	T34513	151618	T29757	F75518	T19431	T45025	T29018	S27923	S50125	S22456	T16543	S23760	A53577	506733	T34434	72
	DB	7	~	N	N	~	~	7	~	П	~	~	~	~	~	7	~	~	~	~	7	~	7	~	~	7	~	~	~	7
	Query Match Length	3020	1664	1489	1274	1188	2187	1367	1151	1344	1229	489	7962	761	3507	990	6642	839	971	3570	801	924	379	.350	856	875	1630	620	2232	873
ď	Query Match	20.6	18.3	16.5	15.6	15.2	15.1	14.8	13.0	12.9	12.8	12.3	12.3	12.3	12.2	12.2	12.1	12.1	12.0	12.0	11.8	11.8	11.7	10.9	10.8	10.8	10.8	10.7	10.6	10.6
	Score	1062.5	942	853	802	784	776	763	671	667	659.5	633	632.5	632	629	626.5	625	622.5	620.5	617	607.5	607.5	605	559.5	556.5	556.5	555.5	551	549	545
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hydroxyproline-ric	extensin precursor	hypothetical prote	exo-alpha-sialidas	calclum-binding pr	hydroxyproline-ric	vsaA protein precu	membrane glycoprot	neurofilament trip	hypothetical prote	membrane glycoprot	mucin FIM-C.1 - Af	interspersed repea	neurofilament trip	mucin-like glycopr
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542	533	532	530.5	530	522	518	518	518	517.5	512.5	509.5	505	504.5	504
30	32	33	34	32	36	37	38	33	40	41	42	43	44	45

ALIGNMENTS

RESULT MA332 MA4332 MA4312 MA4312 MA4312 MA4312 MA4312 MA4312 MA4312 MA4312 MA4313 MA512 MA512
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J. Clin. Invest. 87, 77-82, 1991 A; Title: Human bronchus and intestine express the same mucin gene. A; Reference number: A61257; MUID: 91086481 A; Accession: A61257 A; Status: not compared with conceptual translation	Qy 513 512 Db 1820 NISCRATMYPDVPIGQLGQTVVCDVSVGLICKNEDQKPGGVIPMAFCLNVEINVQCCECV 187' Qy 513 TAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKPAPT-TPKGTAPTTPKE 565	
Molecule type: mRNA Residues: 'T',1925-1948,'T	1880	
	QY 566 PAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTST-TSDKPAPTTP	7TTKGPTST-TSDKPAPTTP 624
keierence number: ryusze; Accession: PQ0328 Molecule type: mRNA Residues: 2328-2468 <xug></xug>	OY 625 KETAPTTPKEPAPTTPKKPAPTTPETPPTTSEVSTPTTKEPTIHK	APTTPETPPPTTSEVSTPTTKEPTIHK 672
A;Cross-references: GB:M86523 A;Experimental source: small intestine A;Accession: P00329 A;Molecule type: protein	QY 673 SPDESTPELSAEPTPKALENSPKEPGVPTTKTPAATKPEMTTAKDKTTERDLRTTPETT 1 1 1 1 1 1 1 1 1	MITTAKDKTTERDLRTTPETT 732 : : STPTAPTTTSGGHTLSPPPST 2115
A;Residues: 2328-2342,'K',2344-2354 <xug1> C;Genetics: A;Gene: GDB:MUC2 A;Cross-references: GDB:120203; OMIM:158370</xug1>	QY 733 TAAPKMTKETATTTEKTTESKITATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTT	FKITTLKTTTLAPKVTTT 789
A;Map position: 11p15.3-11p15.3 C;Superfamily: von Willebrand factor; von Willebrand factor type A repeat homology; von C;Keywords: glycoprotein; intestine; tandem repeat F;2766-2834/Domain: von Willebrand factor type C repeat homology <vwc></vwc>	QY 790 KKIITTEIMNKPEETAKPKDRAINSKATTP :	TAKPKDRATNSKATTP 820 :
Query Match 20.6%; Score 1062.5; DB 2; Length 3020; Best Local Similarity 29.2%; Pred. NO. 4.2e-38; Match 23.7. Concernation 71, Mismatches 447, Indale 315. Gans 30.	OY 821 KPOKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRP 1 1 1 1 1 1 1 1 1	4PELNPTSRIAEAMLQTTTRP 880 : : : ; :
FKYTTPDTSTTQHNKVSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETTVETK 88 i:	QY 881 NQTPNSKLVEVNPKSEDAGGAEGETPHMLL Db 2279 NNTVEIVKVECEPPPMPTCSNGLQPVRVEDPDGCCWHWECDCXCTGWGD-PHXVTFDGLX	AEGETPHMLL 910 : : CCYCTGWGD-PHYVTFDGLY 2337
89 ET-TTINKQTSTDGKEKTTSAKETQSIEKTSAKD 1292 STVLSTTPKLCCLWSDWINEDHPSSGSDDGDREFFDGVCGAPEDIECRSVKDPHLSLEQH	OY 911RPHYEMPEYTPDMDYLPRVPNQGIIIN 937	
QY 122	RESULT 2 T18262 S-layer protein - Clostridium thermocellum	
OY 138 TTTKGPALTTPKEPASTTPKEPASTTPKEPTPTIKSAP-TTPKEPAPTTKSAPTTPKE 196 11	<pre>C;Specias: Lostingum Cheinoceilum C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T18262 F;Fujino, T.; Beguin, P.; Aubert, J.P. T;Fujino, T.; Beguin, P.; Aubert, J.P. T; Pasterio, 175 1801-1809 1903</pre>	9
QY 197 PAPTITKEPAPTITKEPAPTITKSPAPTITKSAP-ITPKEPAPTIPKKPAPTITKKPAPTI 255	A. Hitle: Organization of a Clostridium thermocell e. A. Rieterence number: 218847; MUID:93209931	um gene cluster encoding the cellulo
OY 256 TPKEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAPTTPKEPAPTTTKEP 315	A;Accession: ilssoz A;Accession: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-1664 <fud.) A:Cross-references: FMRI:X67506: NID:a296879; PID:a296881; PIDN:CAA47841.</fud.) 	вJ :G296881; PIDN:CAA47841.1
316	Query Match 18.3%; Score 942; DB 2; Best Local Similarity 33.0%; Pred. No. 3.2e-33; Matches 776; Concernative 83. Mismatches 312.	2; Length 1664; 33; 317 Indels 166; Gabs 43:
3/4 PARPATITE AND THE PROPERTY OF THE PROPERTY	IKGPALTTPKEPTPTP IKGPALTTPKEPTP IKGPALTTPK	
APITPEKPAPITPEELAPITPEEPAPITPEEPAPITPKAAAPITPKEFAFIT 	187 TKSAPTTPKEPAPTTTKEPAPTTPKEPA	
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Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
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A; Reference number: 220986
A; Accession: T31108
A; Accession: T31108
A; Molecule type: DNA
A; Residues: 1-1489 GGDE>
A; Cross references: EMBL: AF061185; NID: 93851513; PID: 9360 C; Genetics: A; Gene: Car90
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Pred. No. 1.7e-29;
5; Mismatches 475
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C;Date: 05-Mar-1995 #sequence_revision 12-May-1995 #text_change 29-Oct-1999
C;Accession: A.9915
S;Rubinstein, A.L.; Broadwater, A.H.; Lowrey, K.; Bedinger, P.A.
S;Rubinstein, A.L.; Broadwater, A.H.; Lowrey, K.; Bedinger, P.A.
A;Description: Pex genes: pollen-specific genes with extensin-like domains.
A;Reference number: 549915
A;Retcon commber: 549915
A;Status: preliminary
A;Mollecule type: DMA
A;Residuses: 1-1188
A;Residuses: 1-1188
A;Cross-references: EMBL:234465; NID:g600117; PIDN:CAAB4230.1; PID:g600118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  975 PPTPVKNPVKKWKPPWEDDDEPAEPVSAPEPEKKTPVLAKKAPAKPRDP---SPKKAAPV 1031
                                                                                                                                                                                                                                                                                                                        1090 TKPDSEAAADPVSGPTSKDPKLSKKAPVEKPRTTDPKDDKLKPSPAKKPEKAPEPAAPK 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 ----LAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTTKSAPTTPKEPA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      738 MTKETATITEKTIESKITATITQVISTITQDITPFKITILKITILAPKVITIKKIITIE 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDISKETSLIVNKETIVETKETITINKQISIDGKEKITSAKETQSIEKTSAKDLAPISKV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APTIPKEPAPTIPKEPAPTITKEPSPITPKEPAPTITKSAPITIKEPAPTITKSAPTIPK 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPSPTTTKEPAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTTTKKPAPTAPKEPAP 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 PTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRPSL----PPN 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----SPSPPPVKTTSPPAPIG----SPSPPPVSVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPPPPVKSPPPPAPVGSPPPPEKSPPPPAPVASPPPVKSP--PPPTLVASPPPVKSPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        460 PTPHSPPAD------DYVPPTPPVPGKSPPATSPSPOVOPPAASTPPPSLVKLSPPQ
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                                                                                                                                                                                                                                                          V------PTTKTPAAT-----KPEMTTTAKDKTTERDLRTTPETT--TAAPK
                                                                                                                           647 TPETPPPTTSEVSTPTTTKEPTTIHKSP----DESTPELSA-EP---TPKALENSPKEPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMNKPEETAKPKDRATNSKATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       1150 KWKPVWDDDPDEPEADFTVPAPSKKPDTEDPADPLG------GPKTKDPK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 15.2%; Score 784; DB 2; L. Best Local Similarity 29.9%; Pred. No. 1.2e-26; Matches 230; Conservative 59; Mismatches 359;
   --TTSDKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | | |:| : |
1244 ADFTMPAPKKPDTEDP 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               849 ---TTPTPRKMTSTMP 861
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604 APTTTKGPTS--
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                                                                                                                                                              Riceimbach, D.
Submitted to the EMBL Data Library, January 1996
A; Description: The sequence of C. elegans cosmid F35A5.
A; Reference number: 218485
A; Accession: T16521
A; Accession: T16521
A; Accession: T16521
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1274 < LEI>A; Residues: 1-1274 < LEI>A; Experimental source: strain Bristol N2; clone F35A5
C; Genetics: Scarrian Bristol N2; clone F35A5
A; Genetics: A; Map position: X
A; Nature Na
A; Map position: X
A; Nature Na
A; Nature Na
A; Na
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26;
                                  hypothetical protein F35A5.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     866 PSPKKAEPNSPVVP----PTPVKNPVKKW-KPPWEDDDEPTEEVKKPSE--PEKKTPVLA 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             334 TIKEPAPITIKSAPTIP-KEPSPITIKEPAPITPK--EPAPITPKKPAP--TIPKEPAPI 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               692 PEKK-TPVLAKKAPTKPDSEAAADPVSGPSSKDPKLAKKAPVKPRDPSPMKAVPIKPAPK 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            389 ТРКЕРАРТТТККРАРТА-РКЕРАРТТРКЕТАРТТРККІТРТТР----ЕКІЛАРПТРЕКРА 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAPITPKETAPITPKGTAPITLKEPAPITPKKPAPKELAPI-TTKEPISTTSDKPAPITP 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             556 KGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPT-----TPKKPAP-----KEL 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    274 KNPTKKWKPPWEDETPVEEVKEPPVPEKKAPVLKKKDPAPAAKARDPSPSKAAPKKVEPS 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                394 PKKAAPAVKPRDSSPKKATPLQADPKAQEVPPTPVKNPVKKYKPPWEVDDEDPVEEVKQP 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEPTPTTP----KEPASTTPKEP----TP-TTIKSAPTTPKEPAPTTTKSAPTTPKEPAP 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----PITPKEPAPTIKEPAPT-----TIKSAPITP 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  234 KEP----APTTPKKPAPTTPKE----PAPTTPKEPTFTPKEPAPTTKEPAPTTPK-EP 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              284 APTAPKKPAP-----TTPKEPAPTTPKEPAPTTTKEP----SPTTPKEPAPTTTKSAPT 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    334 SPVVPPTPVKNPVKKYKPPWEVDDEPAEEVKKPSAPEKKTPVLKRKEPEPSSTTPSSDPS 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            633 APAAVKKPEPISKPKDTAPKKAEPNSPVVP-PTPVKNPVKKWKPPWEDDDAPAKPVSLPE 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 KNRTKK-KP----TP-----KPPVVDEAGSGLDNGD----FKVTTPDTSTTQHNKVSTS 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110 ETQSIEKTSAKDLAPTSKVLAKPTPKAE----TTTKGPA-----LTTP
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                                                                                                                                     Accession: T16251
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Glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - yeast (Saccharomyces cerevisiae)
N.Alternate names: extracellular glucoamylase; mucin-like protein MUC1; protein YIR01
(Speciaes: Saccharomyces cerevisiae
C.Date: 10-Sep-1999 #sequence_revisiae
C.Date: 10-Sep-1999
C.Date: 10-Sep-1999 #sequence_revisiae
C.Date: 10-Sep-1999
C.Date: 
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                                                                                                   GGVTAVPPEISLPPKETPQNATPNESLAASSOKRSPKTSVPKETPPGGVTAMPLEIPSAP 1149
                                                                                                                                                                                     1323 KKTPKTAVPKETSAPSEGVTAVPLEIPPSPRKAPKTAAPKETPAPS--PEGATTAPVQIP 1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1381 PSPRKGSKKAGSKE-TPTTPSPEGVTAAPLEIPISSKKTSKMASPKETLVTPSSKKLSOT 1439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1440 VGPKETSLEGATAVPLEIPPSHKKAPKTVDPKQVPLTPSPK-DAPTTLAE-SPSSPKK-A 1496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1612 T--SLAQTAPPSLQKAPSTTIPKENLAAPAV----LPVSSKSPAAPARASASLSPATAAP 1665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1033 APKTAVSKEIPSKGVTAVPLEISLPLKETSKSATPGEKSASSPKRSPKTAGPKE---TPP 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  654
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                                                                                                                                                                                                                                                                                         TTKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEK-PAPTTPEELAPTTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPTPTT - - - - - - PEEPAPTTPKAAAPNTPKEPAPTTPKE - PAPTTPKEPAPTTPKETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                828 APKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPNQTPNSK
                                                        KEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTT--PKEPAP----TTPKEPAPTT
                                                                                                                                                                                                                                                     358 TKEPAPTTPKEPAPTTPKKPAPTT--PKE-------PAPTTPKEPAP-----T
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                                                                                                                                                      312 TKEPSPITPK-----EPAPTITKSAPTITKEPAPTIT-KSAPTIPK------EPSPTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PITPKGTAPTILKEPAPTTP---------KKPAPKELAPTTTKEPTS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    768 DITPFKITILKTITLAPKVTITKKTITTTEIMNKPEETAKPKDRAINSKATTPKPQKPTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1753 DSHISPVS-DACSTGTTTP 1770
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;Introns: 24/1; 1996/1; 2024/3; 2050/3; 2099/3; 2142/3; 2183/3
;Note: differential splicing converts alphaNAC into a tissue-specific DNA-binding activ
;Keywords: alternative splicing; DNA binding; transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nascent polypeptide-associated complex alpha chain, muscle splice form gp220
                                                                                                                                                                                                                                                                            N;Alternate names: alpha-NAC protein
C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 24-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                            1001 MSSPPPPEVKSPPPPAPVSSPPPPVKSPPPPAPVSSPP---PPVKSPPPPAPVSSPPPV 1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LKE---PA-----PITPKK----PAPKELAPTITKE---PISITSDKPAPTIPKGTAPTIP 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             914 MISKKATEIAASKDVSPSQFPKEVPLLQHVPPTSPPKSPVSDTLSGALTSPPPKGP-PAT 972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----TPKEPAPTTPKK-PAPTTPKEPAPTTP 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTT------PKEPTPTT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IKSAPTTPKE-PAPTTTKSAPTTPK------EPAPTTKEPAPTTPKEPAPTTTKEP 221
PPAPLSSPPPAPQVKSSPPPVQVSSP-PPAPKSSPPLAPVSSPPQVEKTSPPPAPLSSPP 827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                   TIPKETAP----TIP----KKLIPTIPEKLAPTIPEKPAP-----TIPEELAPTIPEEPI
                                                                               -KEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTKGPTSTTSDKPAPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                             -TPKETAPTTPKEPAPTTPKKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; DB 2; Length 2187; 4.6e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAEPTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPET 731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative 122;
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Best Local Simi
Matches 288;
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nuclear antigen, HMNA,
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C;Species: Gallus gallus (chicken)
C;Accession: T18335
R;Shimada, K.; Harata, M.; Mizuno, S.
J. Cell Sci. 110, 3031-3041, 1997
A;Title: A nuclear matrix-associated high molecular mass nuclear antigen, HM A;Reference number: Z18955; MUID:9803440
A;Reference number: Z18955; MUID:9803440
A;Accession: T18535
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1151 cSHL
A;Cross-references: EMBL:D88440; NID:d1177138; PID:d1025045; PIDN:BAA24137.1
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SAPVT----SSTTESSSAPVT----SSTTESSSAPVPTPSSSTTESSSAPVPTPSSSTTE 731
                                                                                                                                                                                                                                                                                      697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      758 --TTQVTSTTTQDTTPFKITTLKTTTLAPKVTT---TKKTITTT-EIMNKPEETAKPKDR
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                                                                                                                                                                       588 KEPAPITPKKPAPKELAPITTKGPTSTTSDKPAPTTPKETAPTTPKEPAP-----TTPKK
                                                                                                                                                                                                                             SAPVPTPSSSTTESSVAPVPTPSSSSNITSSAPSSTPFSSSSTESSSVPVPTPSSSTTESS
                                                                                                                                                                                                                                                                                         PAPTTPETPPPTTSEVSTPT----TTKEPTTIHKSPDESTPELSAEPTPKALENSPKEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSQTETSVSSTTETTIVPTKTTTSVTTPSTTTITTTVCSTGTNSAGETTSGCSPKTVTTT
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                                                           532 KELAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAP---TTPKEPAPT-TPKGTAPTTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KMTSTMPELNPTSRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1123 GTGEYTTEATTLVTTAVTTTVVTTESSTGTNSA-GKTTTGYTT 1164
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Best Local Similarity 25.9%; Préd. No. 7.3e-22;
Matches 284; Conservative 100; Mismatches 419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FMPEVTPDMDYLPRVPNQGIIINPMLSDETNICNGKPVDGLTT
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                                   A;Molecule type: DNA
A;Residues: 1-242 XYAM>
A;Cross.references: EMBE:M16164; NID:g172522; PIDN:AAA35014.1; PID:g172525
A;Accession: B26877
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.8%; Score 763; DB 1; Length 1367; 28.5%; Pred. No. 1.1e-25;
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A. Molecule type: mRNA
A. Residues: 1-19.29-155, P'.157-175, P'.177-182, A'.184-212,1033-1037, A'.1039-1344 <
A. Cross-references: EMBL: X52229; NID: 937053; PIDN: CAA36478.1; PID: 937054
R. Abe, M.; Siddiqui, J.; Kufe, D.
B. Gochem. Blophys. Res. Commun. 165, 644-649, 1989
A. Title: Sequence analysis of the 5' region of the human DF3 breast carcinoma-associa
A. Accession: A36735
A. Reference number: A36735; MUID: 90088473
A. Residues: 1-142, O'. 144-162, O'. 164-168 < ABE>
A. Residues: 1-142, O'. 144-162, O'. 164-168 < ABE>
A. Cross-references: EMBL: M31823; NID: 9181542; PIDN: AAA35757.1; PID: 9181543
R. Masuawa, Y.; Mayenchi, T.; Hamanoue, M.; Ando, S.; Yoshida, J.; Takao, S.; Shimazu
A. Title: A novel core protein as well as polymorphic epithelial mucin carry peanut ag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental Source: gastric carcinoma cell
R; Zrihan-Licht, S.; Baruch, A.; Elroy-Stein, O.; Keydar, I.; Wreschner, D.H.
FEBS Lett. 356, 130-136, 1994
A; Title: Tyrosine phosphorylation of the MUC1 breast cancer membrane proteins cytokin A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Note: undetermined tyrosine residues in the carboxyl-terminal non-repetitive region C;Comment: This protein is length polymorphic. Individuals may have between 21 and 12 partial repeats. The repeat shown is defined by Smal nuclease sites. C;Comment: Serine and threonine residues in the tandem repeat domain are extensively C;Comment: For an alternative splice form without a tandem repeat domain, see PIR:S48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-19, 29-155, 'p', 157-175, 'p', 177-182, 'A', 184-212, 1033-1344 <WRE>
A; Cross-references: EMBL: X52229; NID: 937053
R; Wreschner, D.H.
Submitted to the EMBL Data Library, March 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: PX0066
A;Molecule type: mRNA
A;Residues: 998-1011, ES',1014-1017;1018-1032,'T',1034-1037;1038-1057 <MAS>
                               A; Mestdues: 1-952,1033-1344 <LIG1>
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A; Accession: S40293
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N'Alternate names: breast carcinoma-associated DF3 antigen; core protein KP39; episialin
ncreatic mucin; polymorphic epithelial mucin (PBM)
N'Contains: mucin 1 precursor, epithelial tumor antigen splice form; mucin 1 precursor,
C;Species: Homo saplens (man)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Jun-2000
C;Accession: A35175; B35175; A35886; A35887; S.10572; S40293; A36735; PX0066; S10218; S51
N;Ligtenberg, M.J.L.; Vos, H.L.; Gennissen, A.M.C.; Hilkens, J.
J. Biol. Chem. 265, 5573-5578, 1990
A;Title: Epislalin, a carcinoma-associated mucin, is generated by a polymorphic gene enclassion number: A35175; MUID:90202794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --- 1104
                                                                                                                                                          307 P---APTITKEPSPTTPKEPAPTTTKSAPTTTKEPAP---TTTKSAPTTPKEPSPTTKE 360
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-TAGAVPKASTGTTPAAAPQQPVP---KAAPVTPPSPQQAVPRAATAAA----APVTPQQ 448
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                                                                   251 ЕРАРТТРКЕРТРТ----РКЕРАРТТКЕРАРТТРКЕРАРТАРККРАРТТРКЕРАРТТРКЕ 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  688 TLMAPMGAANTQMAPIGAAGAAQTAPMGAAHTHVSPMGAGGATQMSPTGAANTHMSPIGA 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            653 PTTSEVSTPTTTKEPTTIHKSPDESTPEL--SAEPTPKALENSPKEPGVPTTKTPAATKP 710
                                                                                                                                                                                                          449 PVTKAATTTNATPPPQPIPKAATTTTATPVTPQQPIPKAGTDAAPPPAVPKAPSDGRAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      628 LPSSPVASAMHAKVTPRPLPASPVPMAASPASLGPDAARVALATNAASPGAKPEAAGGNG
                                                                                                                                                                                                                                                                                                                                                                                             569 KPVPLMALTPQPVTAQMVTQLAATKPSPIVPKASPK-ALMTPPPPPPGLPRALAAAKLLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----TPKGTAPT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                976 IGVTEASPSADGARLSPGPTAATDGPKASPAATADVTEAATD--VTAAATAVPA----EA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        830 KKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPNQTPNSKLV
                                                                                                                                                                                                                                                      361 Р----АРТТРКЕРАРТТРККРАРТТРКЕРАР------ТТРКЕРАРТ-ТТККРАРТАР
                                                                                                                                                                                                                                                                                                                                                  K-----EPAPTTPK---ETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   612 ----TSTTSDKP-APTTPKET---APTTPKEP---APTTPKKP-APTTPETPP----
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enetics: sene: GDB:MUC1; PUM	: :
	QY 676 ESTPELSAEPTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERD 724
<pre>(eywords: alternative splicing; duplication; glycoprotein; phosphoprotein; polymorphis -1344/Product: mucin 1 precursor, splice form A *status predicted <prea> -62/Region: mucin 1 amino-terminal non-repetitive -23/Pomain: signal sequence #link PREA *status predicted <siga></siga></prea></pre>	QY 725 LRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTSTTQDTTPFKIT 775 1 1 1 1 1 1 1 1 1
19,29-32/Domain: signal sequence #link PREB #status predicted <sigb> -19,29-1344/Product: mucin 1 precursor, splice form B *status predicted <preb> -19,29-12,1033-1344/Product: mucin 1 precursor, epithelial tumor antigen splice form :38-1017/Region: 20-residue repeats (GSTAPPAHGVTSAPDTRPAP)</preb></sigb>	QY 776 TLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPOKPTKAPKKPT 833 :
143-1344/Region: mucin 1 carboxyl-terminal non-repetitive 1245-1272/Domain: transmembrane #status predicted <trn- #status="" 1246-1272="" <pre="" domain:="" predicted="" transmembrane=""></trn->	QY 834 STKKPKTMPRVKRPKTTPTPRKMTSTMPBLNPTSRIAEAMLQT-TTRPNQTPN 885
	QY 886 SKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLSDETN 945
Atches 305; Conservative //; Mismatches 459; Indels 250; Gaps 50; 77 LTVNKETTVETKETTINKQTSTDGKEKTTSAKETQSIEKTSAKD-LAPTSKVLAKPT 133 11	Qy 946 ICNGRPVDGLTTLRNGT 962 : Db 1050 ASGSASGSASTLVHNGT 1066
134 P-KAETTTKGPALTTPKEPTPTTPKEPASTTPKE 166 :	RESULT 10 T25697 hypothetical protein F16F9.2 - Caenorhabditis elegans
	C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000 C;Accession: T25697 R:Fulton, B.
PTTPKEPAPTTTKEPAPTTTKSAPTTPKEPAPTTPKKPAPTTPKEP	submitted to the EMBL Data Library, August 1996 A; Description: The sequence of C. elegans cosmid F16F9. A; Reference number: 220071 A; Accession: T25697
253APTTPKEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPK 289	A, Status: preliminary: translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Residues: 1-1229 <ful> A; Residues: 1-1229 <ful> A; Cross.references: EMBL: 167956; PIDN: AAB07691.1; GSPDB:GN00028; CESP:F16F9.2</ful></ful>
290 KPAPTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPTT 342	A; Experimental source: strain Bristol N2; Clone Fibry C; Gene: CESP:F16F9.2 A; Map position: X A; Map posit
343 TKSAPTTPKEBSPTTTKEPAPTTPKEPAPTTPKKPAPTTPKEPAPTTPK- 391 1	2; Length 1229; 1;
392EPAPTTTKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPE- 447	33
	DD 119 KVTTSTDASTTNAPTTGKDSTTPEIITGIVVINSKSESVTDMSTTRESTTLSPTTELLTS 178 O1 VERHAUTERMORDHANNAMORGHOGERMAGAKFHOGIRKFGAKDIADFGKVIAKPTDKREHTT 140
485 HGVISAPDIKRAPGSIAPPAHGVISARDIKRAPGSIAPRAHGVISARDIKRARGSIARRA 344 488EPAPTIPKEPAPTIPKETAPTIPKGJAPTILKEPAPTIPKKPAPKEL 534	PETLYSTDSSIST-EQTSPDNTTEIASPMETNTTEATTTSVEPSVSTLASEDETTY
545 HGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGST 600 535 APTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLK 588	QY 141 KGPALTTPKEPTPTPKEPASTTPKEPTPTTIKSAPTTPKEPAPTTTKSAPTTPKEPAPT 200 :
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589 EPAPTTPKRPAPKELAPTTTKGFISTTSDKPAPTTPKETAPTTP 632	
633 KEPAPTTPKKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPD 675	Db 325 THFPVTGTTPNFDTATETPFVAKSEDKMTLSKTAATETTQQTTEVT-DGPEKETTKNV 381

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A.Accession: S24155
A.Status: preliminary
A.Status: preliminary
A.Molecule type: mRNA
A.Residuas: 326-489 CAR2>
A.Cross-references: EMBL:X86030; NID:g791149; PID:g791150
C.Genetics: Ext266
C.Superfamily: hydroxyproline-rich glycoprotein
C.Superfamily: hydroxyproline-signal sequence #status predicted <S1G>
C.Superfamily: signal sequence #status predicted <AM7>
F;14-3409/Product: extensin class 1 #status predicted <AM7>
Reference number:
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A; Residues: 1-489 <ARG>
A; Residues: 1-489 <ARG>
A; Cross-references: EMBL: X91836; NID: 91015936; PIDN: CAA62943.1; PID: 91015937
A; Experimental source: sub_species Red caloona
B; Arsenijevic-Maksimovic, I.; Broughton, W.J.; Krause, A.
Submitted to the EMBL Data Library, April 1995
A; Description: A class of root-hair specific extensins involved in rhizobium/legume inte
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                                                                                                                                                                                                                                           420 TIPKKLIPTTPEKLA---PTTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPTTPKAAAPN 476
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                                     382 SIEIPITIVPLVETISTISTASKESDGFHTTLKLKVTTADSDSTESATTVKPFNEETTTK 441
                                                                                          ---TTPK 383
                                                                                                               384 E-----PAPTTPKEPAP----TTTKKPAPTA--PKEPAPTT---PKETAP 419
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        ----PSPTTPKEPAPTTTKSAP-----TTTKEPAPT----TTKSAPTTPKEPSPTTK 359
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Cispecies: Home sagistes (man)
Cipate: 29-May-1998 #text_change 21-Jul-2000
Cipate: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
Cipate: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
Cipate: 29-May-1998 #sequence_revision 138346
Ritabeit, S.; Kolmerer, B.
Science 270, 293-296, 1995
A; Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.
A; Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.
A; Reference number: A57430; MUID:96026330
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: 17962 <RES>
A; Cross-references: EMBL:X90569; NID:g1017427
C; Genetics:
                                                                     7;
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                                                                                                                                    179 PKEPAPTTTKSAPTTPKEPAPTTTKEPAPTTPKEPAPTTTKEPAPTTTKSAPTTPKEPAP 238
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                                                                                                                                                                                                                                                                                                        84 PSPSPPPYVYKSPPPPSPSPSPPPPYYKSPPPPS--PSPPPPYYKKSPPPPPYY 141
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                                                                  44;
   Length 489;
                                                                     Indels
Query Match
12.3%; Score 633; DB 2; L
Best Local Similarity 31.2%; Pred. No. 1.4e-20;
Matches 149; Conservative 33; Mismatches 252;
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A;Cross-references: GDB:127867; OMIM:188840
A;Map position: 2q31-2q31
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Length 7962;

DB 2;

12.3%; Score 632.5;

Mon Apr 29 08:35:35 2002

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hypothetical protein At2g27380 [imported] - Arabidopsis thaliana C.0*****
hypothetical protein At2g27380 [imported] - Arabidopsis thaliana (Gouse-ear cress)
C.Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C.Accession: C84672
R.inin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, A.; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A; Accession: C84672
A; Reference number: A84420; MUID:20083487
A; Accession: C84672
A; Analecule type: DNA
A; Residues: 1-761 < C$TO>
A; Crouetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 PPTPIYSPPIKPPVHKPPTPIYSPPVKPPPVQTPPTPIYSPPVKPPPVHKPPTPTYSPP 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421 KLPPUKPPTPIYSPPUKPPPUHKPPTPIXSPPUKPPPT 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               878 TRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIIN 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 PTPKAETITKGPALITP---KEPIPT-TPKEPASITPKEPTPITKSAPTIPKEPAPITT 187
                                                                                                                                                                                                                                KAPKKPTSTKK-----PKTMPRVRK---PKT-TPTPRKMTSTMPELNPTSRIAEAMLQTT 877
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                                                                                 767 QDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQKPT
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                                                                                                                                                           6877 VPEVPKKVE--EKRIILPK----EEEVLPVEVTEEPEE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------PPAKGRTVLEEKVSVAFR 7021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           938 PMLSDETNICNGKPVDGLTTLRNGTLVAFR 967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: At2g27380
A; Map position: 2
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OY 503 KETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAP 560 Db 481 TYSSPVOPPPVOKPPTPTSPPDTFSPPTFSPPTFSPPTFSPPTFSPPTFSPPT	bb 2294 LSPDVSQSSTTPNNLSESSTVETPKTSSEVSLNSEEPSTTEAPTTLSPDILSTTTN 2349
561 TTPKEPAPTTPKEPAPT-TPKGTAPTTLKEPAPTTPKKPAPKELAPTTKGPTSTTSD :	Qy 398
618 KPAPTTPKETAPTTPKEPAPTTPKKPAPT-TPETPPPTTSFENGFFFUNFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	OY 428 TTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPTTPKAAAPN 476 1. : : : : : : : :
DESTPELSAEPTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTA	Oy 477 TPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTP 510
APKMTKETATTTEKTTESKITATTTQVTSTTTQDTTP 771	QY 511 KGTAPTILKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKPAPT 553 1 : :: :
RESULT 14	Qy 554TPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPT 593 b 2583 SEIEAITSNTPFKQGRTPITTSPKSLVKSTTSPSTVTSSEPSESTKRTTVSTTVSTTTPT 2642
hypothetical protein ZK783.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999	Qy 594 TPKKPAPKELAPTTTKGPT-STTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPTTPETPP 652
C. Arcesszon: 194313 R. Favello, A.; Vaudin, M. Submitted to the EMBL Data Library, August 1994 A. Description: The sequence of C. elegans cosmid ZK783.	QY 653 PTTSEVSTPTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPTKTPAAT 708 : :
A; Accession: T34513 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Doction: 1-3507 / DNA	QY 709 KPEMTTTAKDKTTERDLRTTPAPKMTKETATTTEKTTESKITATTT 759 DD 2753 KLSSLFPESITSEAVTVSSRAPAEITMSSESHREISTVSSEPSEPEIPLSTTVSPN 2808
A: Kestudes: 1.307 cray. A: Kestudes: 1.307 cray. A: Cross references: EMBL:U13646; PIDN:AAC24418.1; GSPDB:GN00021; CESP:ZK783.1 A: Experimental source: strain Bristol N2; clone ZK783 A: Genetics:	Qy 760QVTSTTTQDTTP-FKITTLKTTTLAPKVTTTKKTITTEIMNRP 802 : :
A; Wap position: 3 A; Map position: 3 A; Introns: 14/1; 48/2; 84/1; 196/3; 303/1; 381/1; 586/1; 605/1; 1175/3; 1207/1; 1409/2; 3504/1	QY 803 EFTAKPKDRATNSKATTPKPOKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMIST 859 1
Query Match 12.2%; Score 629; DB 2; Length 3507; Best Local Similarity 24.1%; Pred. No. 1.2e-19; Matches 252; Conservative 158; Mismatches 416; Indels 218; Gaps 45;	Qy 860 MPELNPTSRIAEAMLQTTT 878
Qy 10 KKKPTPKPPVVDEAGSGLDN-GDFKVTTPDTSTTQHNKVSTSPKITTAK 57 : :	RESULT 15 151618 nucleolar phosphoprotein - African clawed frog
QY 58 PINPRPSLPPNSDTSKETSLTVNKETTV-ETKETTTTNKQTSTDGKEKTTSAKETQS 113 1	<pre>C:Species: Xenopus laevis (African clawed frog) C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 24-Sep-1999 C:Accession: 151618; S57757 R;Cairns, C.; McStay, B.</pre>
QY 114 IEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTP 169 2061 ITESSVKSTTPKEESSSEITVKLSSKSPEVTESSVKSSPSTPS-TTSQSVTSTVPETSKS 2119	J. Cell Sci. 108, 3339-3347, 1995 A.Title: Identification and cDNA cloning of a Xenopus nucleolar phosphoprotein, xNopp A.Reference number: I51618; MUD:96019267 A.Accession: I51618
QY 170 TTIKS-APTTPKEPAPTTTKSAPTTPKEPAPTTTKEPAPTTTKEPAPTTTKEPAPTTTKE 228	A.Status: preliminary: translated from GB/EMBL/DDBJ A.Molecule type: mRNA A.Residues: 1-990 (CAI> A.Cross-references: EMBL:X88927; NID:g895920; PIDN:CAA61368.1; PID:g895921
QY 229 APTIPKEBAPTIPKKPAPITPK-EPAPTIPKEPIPTIPKEPAPTITKEP-APTIPKEPAPT 286 2179 ASVAPVKLSSLSPDVSQPSTKIFDATESSTVQASETSSGTSVKSTSEPESHVTKLSIISS 2238	C.Genetics: A.Gene: xNopp180 C.Superfamily: nucleolus-cytoplasm shuttle phosphoprotein C.Keywords: phosphoprotein
QY 287 APKKPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTK 344	atch 12.2%; Score 626.5; DB 2; Length 990; cal Similarity 26.2%; Pred. No. 4.9e-20;
Qy 345 SAPTTPKEPSPTTTKEPAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTT- 397	Matches 253; Conservative 132; Mismatches 393; Indels 187; Gaps 45;

DNKKNRTKKFPPRPPVVDEAGSGLDNGDEKVTTPDTSTTQHNKVSTSPKITTARPINPR 62	R.SAPTTPKEPAPTTPKEPAPTTTKEPAPTTPKEPAPTT-TKEPAPTTT	2 TKEPSPTTPKEPAPTTTKSAPTTTKSAPTTPKEPSPTTTKEPAPTTPKEPA- 370	AANTTEKEPAPTTEKEPAPTTEKEPAPTTEKETAPTTE-KGTAPTTLKEPAPTTEK 52	6 APTTPKK-PAPTTPETPPPTTSEVSTPTTKE-PTTHKSPDESTPELSAEPTPKALENS 693 1
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6 6 6 6 6			60 G G G G G G G G G G G G G G G G G G G	

Search completed: April 26, 2002, 16:18:59 Job time: 329 sec

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14.5
Compugen Ltd.
GenCore version
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OM protein - protein search, using sw model

April 26, 2002, 16:19:21; Search time 47.4 Seconds (without alignments) 748.767 Million cell updates/sec Run on:

Perfect score:

US-09-556-246-1_COPY_200_1167 5155 1 VKDNKKNRTKKKPTPKPPVV......GKPVDGLTTLRNGTLVAFRG 968 Sedneuce:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 segs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ption	000817 homo sapien 006852 clostridium 0068640 saccharomyc P15941 h mucin 1 p 025460 mytilus edu 09493 homo sapien P1998 nicotiana t P19946 mus musculu P20253 trypanosoma 002910 drosophila 025434 mytilus ae 0255434 mytilus ae 0256434 mytilus ae 0256434 mytilus ae 0256434 mytilus norv 056549 komo sapien P14918 zea mays (m 088795 mus musculu P46593 candida alb P4759 saccharomyc P46593 candida alb P37370 saccharomyc P28968 equine herp P41179 saccharomyc P28968 equine herp P41179 saccharomyc P48634 homo sapien P46593 candida alb P37370 saccharomyc P28968 equine herp P41173 xenopus lae P10220 herpes simp 0901100 totalurid h 027409 mytilus gal 000220 homo sapien P10220 herpes simp 09ume homo sapien P27546 mus musculu
SUM	MUCZ_HUMAN SLP1_CLOTM AMYH_YEAST AMYL_YEAST AMOL_HUMAN FP1_MYTED ZAN_HUMAN EXTN_TOBAC NFH_MOUSE FP1_MYTCR CPN_DROME FP1_MYTCR CNOT_WOUSE NFH_HUMAN RPB1_CRANT NFH_HUMAN RPB1_CRANT NFH_HUMAN FP1_CRANT NFH_HUMAN FP1_MYTCR SSP2_FLORA VGC_HSVI TYDZ_HUMAN VGSO_HSVI TYDZ_HUMAN VGSO_HSVI TYDZ_AKENLA T
DB	
Length	5179 1564 1255 1257 200 620 620 1087 1162 1970 1020 267 267 277 1161 1161 1161 1161 217 217 217 217 217 3164
% Query Match	7.24 7.20 7.20 7.20 7.20 7.20 7.20 7.20 7.20
Score	800 8 800 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
Result	1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2

009550 caenorhabdi 010172 schizosacch P28955 equine herp 028983 sus scrofa p54259 homo sapien p54259 homo sapien p34926 rattus norv 0992n3 homo sapien p60131 homo sapien 099618 h nuclear r 013428 homo sapien
YOU3_CAEEL YAV1_SCHPO TEGU_HSVBB ZAN PIG DRPL_HUMAN MAPR_RAT MAPR_RAT NGP3_EBV UGP3_EBV KIG7_HUMAN VGP3_EBV KIG7_HUMAN CCR2_HUMAN
1251 1794 3424 2476 1185 1229 1183 3256 2517
88888877 777888888877 77788888888
422.5 422.5 422.5 419.5 416.5 416.5 411.5 411.5 407.5 405.5
66666666444444446000000000000000000000

ALIGNMENTS

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THEOLOGY OF THE ALM INDICATE AND INTERCEDED AND OTHER MUCUS MEMBRANE-CONTAINING ORGANS. THOUGHT TO PROVIDE A DEPTHER MUCUS MEMBRANE-CONTAINING ORGANS. THOUGHT TO PROVIDE A DEPTHER MUCUS MEMBRANE-CONTAINING ORGANS. THOUGHT TO PROVIDE A PROTECTIVE, LUBRICATING BARRIER AGAINST PARTICLES AND INFECTIOUS CACHERY AT MUCUSAL SURRACES.

1- SUBBINIT: MULTIMERIC.
1- SUBGENTS AT MUCUSAL SECRETED.
1- TISSUE SPECIFICITY: COLON, SMALL INTESTINE, COLONIC TUMORS, BRONCHUS, CERVIX AND GALL BLADDER.
1- PINS: ALL CYSTEILE RESIDUES ARE INVOLVED IN INTRACHAIN OR INTERCHAIN DISULFIDE BONDS (BY SIMILARITY).

1- POLYMORPHISM: THE NUMBER OF REPEATS IS HIGHLY POLYMORPHIC AND VARIES AMONG DIFFERENT ALLEES.
1- SIMILARITY: THE N-TERMINAL DOMAINS SOME SIMILARITY TO THAT OF SILKWORM HEMOCYTIN.

1- SIMILARITY: CONTAINS 2 VWFC DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The human MUC2 intestinal mucin has cysteine-rich subdomains located both upstream and downstream of its central repetitive region."; J. Biol. Chem. 267:21375-21383(1992).
                                                                                                                                                                                                                                                                              TISSUE-Intestine;
MEDILINE-94132002; PubMed-8300571;
MEDILINE-94132002; PubMed-8300571;
Gum J.R. Jr., Hicks J.W., Toribara N.W., Siddikt B., Kim Y.S.;
"Molecular cloning of human intestinal mucin (MUC2) cDNA.
Identification of the amino terminus and overall sequence similarity to preprovon Willebrand factor.";
J. Biol. chem. 269:2440-2446(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1343-1895 AND 4176-4195 FROM N.A.
MEDLINE-91358717; PubMed-1863763;
Toribara N.W., Gum J.R. Jr., Culhane P.J., Lagace R.E., Hicks J.W.,
Petersen G.M., Kim Y.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUB-colon;
MEDLINE=93016075; PubMed=1400449;
Gum J.R. Jr., Hicks J.W., Toribara N.W., Rothe E.-M., Lagace R.E.,
                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                   002817; 014878;
01-JUN-1994 (Rel. 29, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-2001 (Rel. 40, Last annotation update)
MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 626-1895 AND 4196-5179 FROM N.A.
                                 5179 AA.
                                 PRT;
                                 STANDARD;
                                                                                                                                                                  Homo sapiens (Human).
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                 MUC2 OR SMUC.
                                   MUC2_HUMAN
T
HUMAN
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| | | | | | | DHPSSGSDDGDREPFDGVCGAPEDIECRSVKDPHLSLEQHGQKVQCDVSVGFICKNEDQF 1371
                                                                                                                                                                                                                                                                                                                                                                                                         1591 ITTTTPPPTTTPSPPTTTTTPPPTTTPSPPTTTPITPPTSTTTLPPTTTPSPPPTTTT 1650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FSPFSTTTPTTPCVPLCNWTGWLDSGKPNFHKPGGDTELIGDVCGPGWAANISCRATMYP 1829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVPIGQLGQTVVCDVSVGLICKNEDQKPGGVIPMAFCLNYEINVQCCECVTQPTTMTTT 1889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTP 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAP---TTPKEPSP 355
                                                                                                                                                                                                                                                                                                                                                                                                                                    149 KEPT-----PTTPKEPASTTPKEPTPTTIKSAP-TTPKEP-----APTTTKSAP-TTP 194
                                                                                                                                                                                                                                                                                                                                                     -----ITTAKPINPRPSLPPNSDTSKETSLTVNKETTVETK 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PITPKEPAPITPKEPIPITPKEPAPITKEPAPTTPKEP-----APTAPKKPAPITPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            195 KEPAPITIKEPAPITPKEP-----APITIKEPAPITIKSAP--TIPKEPAPITPKKPA
                                                                                                                                                                                                                                                                                                                                                                          GNGPFGLCYDYKIRVNCCWPMDKCITTPSPPTTTPSPPFTTTTLPPTTTPSPPTT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEKPAPTTPEELAPTTPEEPTPT-TPEEPAPTTPKAAAPNTPKEPAPTTPKEP-----AP
                                                                                                                                                                                                                                                                                                              21 DEAGSGLDNGDFK------VTTPDTSTTQH-NKVSTSPK----
                                                                                                                                                                                                                                                                     22.7%; Score 1168; DB 1; Length 5179; 32.5%; Pred. No. 4.8e-39;
                                                                                                                                                                                   H -> L (IN REF. 3).
T -> S (IN REF. 3).
L -> P (IN REF. 3).
M -> T (IN REF. 3).
G -> S (IN REF. 2).
G -> S (MW; 85CD7571F89A5663 CRC64;
                                                                                                                                                                                                                                                                                         53; Mismatches 448;
         N-LINKED (GLCNAC
                                                                                                                                                                                                                                      540295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----KETAPTTP------
                                                                                                                                                                                                                                                                   Query Match 22.7
Best Local Similarity 32.5
Matches 363; Conservative
   4881
4888
4955
4970
5019
5038
1351
                                                   CARBOHYD
CARBOHYD
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InterPro; IPR001000; CR_Cysknot.
InterPro; IPR001007; VWd.
InterPro; IPR001846; Vwd.
IPR011F; SM0014; Vwd.
IPR051TE; SM0011; VWC_def; 2.
IPR051TE; PS01185; CTCK_1; IPR051TE; PS01185; CTCK_1; IPR051TE; PS011208; VWFC; 2.
IPR051TE; PS011208; VWFC; 2.
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VWFC 2.
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EMBL; M74027; AAA59875.1;
EMBL; M94132; AAA59163.1;
EMBL; M94132; AAA59164.1;
MIM; 158370;
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TTPKEPAPT-TPKETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKP
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Bacteria, Firmicutes; Bacillus/Clostridium group, Clostridiaceae;
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01-JUN-1994 (Rel. 29, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN
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Pfam; PF00395; SLH; 3.
PROSITE; PS01072; SLH_DOMAIN;
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MW; 5F396695BA9FE74B CRC64;
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GLY/PRO/SER/THR-RICH.
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Matches 276;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=S288C / AB972;
Barrall B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,
Barrall B.G., Badcock K., Copsey T., Dear S., Devlin K., Fraser A.,
Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones M.,
Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,
Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
Walsh S.V., Whitehead S.,
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                     ------KPTSTPAPTEIE-EPTPSDVPGAIGGEHRAYLRGY------PDGSFRP 1465
             871 EAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLP 927
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PIR; A26877; A26877.

PIR; S48478; M4478.

SGD; S0001458; MuC1.

Hydrolase; Glycosidase; Polysaccharide degradation; Glycoprotein;
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SER/THR-RICH.
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                       Saccharomycetes;
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                                                                                                                                                                   1,4-ALPHA-
                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacch
Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                      01-FEB-1995 (Rel. 31, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
GLUCOAMYLASS 51/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN GLUCOENDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).
STAL OR STA2 OR MAL5 OR YIR019C.
                                                                                                      1367 AA
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                                                                                                    AMYH_YEAST STANDARD; F P08640; P08068; 01-AUG-1988 (Rel. 08, Created) 01-FEB-1995 (Rel. 31, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M16164; AAA35014.1; -.
EMBL; M16165; AAA35015.1; -.
EMBL; X13857; CAA32069.1; -.
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874 874 N-LINKED (GLCNAC. . .) (POTENTIAL).
1367 Aa; 136110 MW; 91C00E2DBD61AA9D.CRC64;
                                                                                                       14.8%; Score 763; DB 1; Length 1367;
ilarity 28.5%; Pred. No. 1.1e-23;
Conservative 98; Mismatches 465; Indels 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                915 FMPEVTPDMDYLPRVPNQGIIINPMLSDETNICNGKPVDGLTT 957
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                                                                                                                                            Best Local Similarity
Matches 286; Conserv
        CARBOHYD
SEQUENCE
                                                                                                                        Query Match
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Biochem. 189:475-486(1990)

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MUCLI, HUMAN STANDARD; PRT; 1255 AA.
P15941; P15942; P13931; P17626; Q14128; Q16442; Q16437; Q9Y4J2;
P15941; P15940 (Rel., 13, Created)
O1-JAPR-1990 (Rel., 14, Last sequence update)
20-AUG-2001 (Rel., 40, Last annotation update)
MUCIN | PRECISTORSOR (POLYMORPHIC EPITHELIAL MUCIN) (PEM) (PEMT)
(EPISIALIN) (TUMOR-ASSOCIATED MUCIN) (CARCINOMA-ASSOCIATED MUCIN)
(TUMOR-ASSOCIATED EPITHELIAL MEMBRANE ANTIGEN) (HAA) (H23AC) (PEBANUT-REACTIVE URINARY MUCIN) (PUM) (BREAST CARCINOMA-ASSOCIATED ANTIGEN)
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may generate multiple protein forms.";
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Wataryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-90276413; Pubbled-2351132; Wreschener D.H., Hareuveni M., Tsarfaty I., Smorodinsky N., Horov J., Zaretsky J., Kotkes P., Weiss M., Lathe R., Dion A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Breast carcinoma;
TISSUE-Breast carcinoma;
MEDLINE-9036815; PubMed-1697589;
Gendler S.J., Lancaster C.A., Taylor-Papadimitriou J., Dubig Peat N., Burchell J., Pemberton L., Lalani E.-N., Wilson D.;
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1123 GTGEYTTEATTLVTTAVTTESSTGTNSA-GKTTTGYTT 1164
                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Biol. Chem. 265:5573-5578(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE-91097524; PubMed-2268309;
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TISSUE-Breast carcinoma;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                TISSUE-Pancreas;
                                                             MUC1_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                     *A highly immunogenic region of a human polymorphic epithelial mucin expressed by carcinomas is made up of tandem repeats."; J. Biol. Chem. 263:12820-12823(1988).
                                                                      Tsarfaty I., Hareuveni M., Horev J., Zaretsky J., Weiss M., Edeltsch J.M., Garnier J.M., Lathe R., Keydar I., Wreschner D.H.; "Isolation and characterization of an expressed hypervariable gene coding for a breast-cancer-associated antigen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACID).
POLYMORPHISM: THE NUMBER OF REPEATS IS HIGHLY POLYMORPHIC. IT
VARIES FROM 21 TO 125 IN THE NORTHERN EUROPEAN POPULATION. THE
MOST FREQUENT ALLELES CONTAINS 41 AND 85 REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. A SECRETED FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-96183746; PubMed-8608966;
Weiss M., Baruch A., Keydar I., Wreschner D.H.;
"Preoperative diagnosis of thyroid papillary carcinoma by reverse
transcriptuse polymerase chain reaction of the MUCI gene.";
Int. J. Cancer 66:55-59(1996).
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-1- TISSUE SPECIFICITY: ABERRANTLY EXPRESSED IN HUMAN EPITHELIAL TUMORS, SUCH AS BREAST CANCER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Lung;
MEDLINE-96181716; PubMed-8604237;
Yu C.J., Yang P.C., Shew J.Y., Hong T.M., Yang S.C., Lee Y.C.,
Lee L.N., Luh K.T., Wu C.W.;
"Mucin mRNA expression in lung adenocarcinoma cell lines and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Abe M., Siddigui J., Kufe D.; Sequence analysis of the 5' region of the human DF3 breast carcinoma-associated antigen gene."; Blochem. Blophys. Res. Commun. 165:644-649(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Breast carcinoma;
Buluwela L., Liu Q., Lugmani Y.A., Gomm J.J., Coombes R.C.;
Submitted (OCT-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                   MEDLINE-88330762; PubMed-3417635;
Gendler S.J., Taylor-Papadimitriou J., Duhig T., Rothbard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-169 FROM N.A. MEDLINE-90088473; PubMed-2597151;
                                       MEDLINE=91033045; PubMed=1688329;
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EMBL; M32738; AAA35804.1; -.
EMBL; M32739; AAA35806.1; -.
EMBL; JO5581; AAA59876.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-109 FROM N.A.
                                                                                                                                                                                                                                                                                                PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-46 FROM N.A.
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                                                                                                                                                                                   coding for a breast-car
Gene 93:313-318(1990).
SEQUENCE FROM N.A.
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290 KPAPITIPKEPAPITPK----EPAPITIKEPSPITIPKEPAPIT---IKSAPITIKEPAPIT 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAPPAHGVTSAPDNRPALGSTAPPVHNVTSASGSASGSASTLVHNGTSARATTTPASKST 990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-MAY-2001 (Rel. 40, Last annotation update)
ADHESIVE PLAQUE MATRIX PROTEIN (POLYPHENOLIC ADHESIVE PROTEIN) (FOOT PROTEIN 1) (MEFP1) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=91025829; PubMed=1367451; Strausberg S.L., Strausberg R.L.; Filpula D.R., Lee S.M., Link R.P., Strausberg S.L., Strausberg R.L.; "Structural and functional repetition in a marine mussel adhesive
                                                                                                                                                                                                                       HGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAP--
                                                                                                                                                                                                                                                                                           AP--TTPKGTAPTTPKEPAPTTPKEPAPTTPKG----TAPTTLKEPAPTTP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            587 APGSTAPPAHGVTS----APDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PDTRPAPGS--TAPPAHGVISAPDIRPAPGSTAPPAHGVISAPDIRPAPGSTAPPAHGVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ::| |: | | : | | | :| SAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAPKMTKETATTTEKTTESKITATTTQVTSTTTQDTTP--FKITTLKTTTLAPKVTTTKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SAP----DIRPAPGSTAPPAHGVTSAPDIRPAPGSTAPPAHGVTSAPDIRPAPGSTAPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              876 HGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAP--GSTAPPAHGVTSAPDTRP---APGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------TSRIAEAMLQ--TTTRPNQTPNSK--
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Sukaryotas, Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilidae; Mytiloidea; Mytiloi
                                                  299 TSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGV
                                                                                                                                      359 T-SAPDT--RPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPA
                                                                                                                                                                                392 ---ЕРАРТТККРАРТАРКЕРАРТТРКЕТАРТТРККІТРТГРЕКLАРТТРЕКРАРТТРЕЕ
                                                                                                                                                                                                                                                                 LAPTTPEEPTPTTPEEPAPTTPKA----AAPNTPKEPAPTTPK----EPAPTTPKEPAPT
                                                                                                                                                                                                                                                                                                                                                   501 TPKETAPTTPKGTAPTTLKEPAPTTP------KKPAPKELAPTTTKEPTSTTSDKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -KKPAPKELAPTTKGPTSTTSDKPAP--TTPK----ETAPTTPKEPAPTTP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --KKPAPTTPETPPPTTSEVSTPTTTKEPTT-----IHKSPDESTPELSAEPTPKALE
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                                                                                            TKSAPTTPKEPSPTTKEP----APTTPKEPAPTTPK----KPAPTTPKEPAPTTPK-
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MISSING (IN SECRETED ISOFORM).
T -> A (IN REF. 11).
P -> Q (IN REF. 9).
P -> Q (IN REF. 9).
P -> Q (IN REF. 9).
A -> T (IN REF. 3).
A -> T (IN REF. 3).
A -> T (IN REF. 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 PGSGSSTTQGQDVTLAPATEPASGSAATWGQDVTSVPVTRPALGSTTPPAHDVTSAPDNK 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 PTPTT-----IKSAPTTPKEPAPTTT-----KSAPTTPKEPAPTTTKEP-----A
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                                                                                                                                                                                                                                                                                                                               InterPro; IPR000082; SEA.
Pfam; PF01390; SEA; 1.
SMRTY; SM00200; SEA; 1.
PROSITE; PS50024; SEA; 1.
Glycoprotein; Signal; Cytoskeleton; Actin-binding; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. . .) (POTENTIAL T -> TATTARKAT (IN ISOFORM B). MISSING (IN ISOFORM C). MISSING (IN ISOFORM D). MISSING (IN POLYMORPHIC EPITHELIA MISSING (IN POLYMORPHIC EPITHELIA
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llarity 27.1%; Pred. No. 2.4e-19;
Conservative 79; Mismatches 437,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTTPKEPAPTTTKEPAPTTTKSAPTTPKEPAPTTP----
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                                                                                                                                        S81781; AAD14376.1; ALT_INIT.
S81736; AAD14369.1; ALT_INIT.
M21868; AAA59874.1; ALT_SEQ.
               ALT_SEQ.
ALT_SEQ.
ALT_SEQ.
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154 154
1021 1021
1251 1251
1255 AA; 122072 M
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               CAA36478.1;
CAA36477.1;
                                                                                                   Z17325; CAA78973.1;
M31823; AAA35757.1;
                                                       AAB59612.1;
                                                                                 CAA78972.1;
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GlycoSuiteDB; P15941; -.
MIM; 158340; -.
MIM; 113720; -.
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PIR; B35175; B35175.
PIR; S10218; S10218.
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               X52229;
X52228;
                                                             M35093;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26;
                                                                Waite J. H.;

"Evidence for a repeating 3,4-dihydroxyphenylalanine- and hydroxyprofine-contraining decapeptide in the adhesive protein of the hydroxyprofine-contraining decapeptide in the adhesive protein of the hydroxyprofine-contraining decapeptide in the adhesive protein of the mussel, Mytilus edulis L.";

J. Biol. Chem. 258:2911-2915(1983).

-I- FUNCTION: PROVIDES ADHESIVENESS TO THE MUSSEL'S FOOT. MUSSELS CHENCION. PROVIDES ADHESIVENES TO THE MUSSEL'S FOOT. MUSSEL'S ADHESIVE IS A BUNDLE OF THERADS, CALLED A BYSSUS, FORNED BY A FIBRONCS COLLAGENOUS CORE COATED WITH ADHESIVE PROTEINS.

-I- SUBCELLULAR LOCATION: SECRETED.

-I- SUBCELLULAR LOCATION: SECRETED THE BYSSAL GLAND.

-I- DOMAIN: ALMOST EXCLUSIVELY COMPOSED OF REPEATS OF A DECAPEPTIDE.

-I- PTM: THE DECAPETIDE A.K.P-S-Y-P-P-T-Y-K IS POST-TRANSLATIONALLY MODIFIED AS FOLLOWING: THE PRIVATH AND SEVENTH RESIDUES ARE HYDROXYLATED AND THE PROVICTIMATE IS A 3,4-DIHYDROXYPHENYLALANINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TANDEM REPEATS OF Y-K-[PA]-K-[LP]-[ST]-Y-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88 KETTTINKQTSTDG--KEKTT---SAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKG 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194 PKEPAPTTTKEPA--PTTPKEPA-----PTTTKEPA-PTTTKSAPTTPK--EPAPTT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143 PALTTPKEPTPTTPKE----PASTTPKEPTPTTIKSAPTTP----KEPAPTTTKSAPTT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSSYKPKKTYPPTYKPKLTYPPTYKPKPSYPPTYKPKPSYPPSYKTKKTYPSSYKAKPSY 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 PKKPA--PTTPKEPA--PTTPKEPT--PTTPKEP---APTTKEPAPTTPKEPA--PTAPK 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          294 KPSYPPTYKAKPSYPPTYKAKPSYPPTYKAKPSYPPTYKAKPSYPPTYKAKPTY 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTTTKSAPTTPKEPSPTTTKEPAPTTPKEPAPTTPKKPA--PTTPKEPA--PTTPKEPAP 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 IQHNKVSTSPKITTAKPINP------RP--SLPPNSDTSKETSLTVNKETTVET 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KPA--PITPKEPA--PITPKEPA--PITTKEPS--PITPKEPA-PITTKSAPITIKEPA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.8%; Score 556.5; DB 1; Length 875; larity 28.7%; Pred. No. 8.9e-16; Conservative 106; Mismatches 375; Indels 195
                                           AND POST-TRANSLATIONAL MODIFICATIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-P-[ST].
; 6EA85312748CAACE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002964; Adhesive_plaq.
InterPro; IPR002965; P_rich_extensn.
PRINTS; PR01216; ADHESIVEI.
PRINTS; PR01217; PRICHEXTENSN.
                lotechnol. Prog. 6:171-177(1990)
                                                         PubMed=6298211:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 875 AA; 100412 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X54422; CAA38294.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    870
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                                        PARTIAL SEQUENCE,
MEDLINE-83135732;
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Matches 272;
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PELLUCIDA
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                                              410 PPTYKAKPTYKAKP-----TYPST-YKAKPSYP----PSYKAKPSYPPTYKAKPTYKA 457
                                                                                                                                                                                                                                                                                                                                                                 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   716 AKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTSTTTQDTTPFKIT 775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                507 PKLIYKPIYK-PKPSYRPSYKPKITYPPIYK-------PKISYPPIYKAKPSY 551
                                                                                                                                                                                                                                                                                                                                                                                                                       611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SUBUNIT: PROBABLY FORMS COVALENT OLIGOMERS.
-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN, EXCLUSIVELY ON THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Large-scale sequencing of two regions in human chromosome 7q22: analysis of 650 kb of genomic sequence around the EPO and CUTL1 loci reveals 17 genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gao Z., Harumi T., Garbers D.L.; "Chromosome localization of the mouse zonadhesin gene and the human
                                                                                                                                                                                                                                 510 PKGTAPITLKEPAPITPKKPAPKELAPITIKEPISITSDKPAPITPKGTAPIT----PKE
                                                                                                                EPTPTTPEEPAPTTPKAAAPNTPKEPAPTTPKEPAPTTPKE----PAPTTPKETAPTT--
                                                                                                                                                                                                                                                                                                                                                                                             458 KPT----YPSTYKA----KPSYPASYKAKPSYPPTYKSKSSYPSSYKPKKTYPPTYK
                                                                                                                                                                                                                                                                                                                                                        PAPITIPKEPAPITIKGT --- APITLKEPA--PITPKKPA--PKELAPITIKG-PISTTSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 612 KAKPSYP----PIYKAKPSYPPIYKAKPTYPSTYKAKPSYPPIYKPKISYPPIYKAKPSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         727 YKAKPIYKAKPIYPSIYKAKP--TYKAKPIYPPIYKAK------PSYPPIYKPKPSYPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQKPTKAPKK---P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            618 KPAPTTPKETAPTTPKEPA--PTTPKKPA-PTT----PETPPPTTSEVSTPTTTKE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTTIHKSPDESTPELSAEPTPKALENSPK----EPGVPTT--KTPA----ATKPEMTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Wakaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_raxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glockner G., Scherer S., Schattevoy R., Boright A., Weber J., Tsui L.C., Rosenthal A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- FUNCTION: BINDS IN A SPECIES-SPECIFIC MANNER TO THE ZONA OF THE EGG. MAY BE INVOLVED IN GAMETE RECOGNITION AND/OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------RKMTSTMPELNPTSR 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       827 STYKLKPSYPPTYKSKTSYPPTYNKKISYPSSYKAKTSYPPAYKPTNR 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Testis;
MEDLINE=97271566; PubMed=9126492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 2338-2700 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last seq
20-AUG-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Res. 8:1060-1073(1998).
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Genomics 41:119-122(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZONADHESIN (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 X HEPTAPEPTIDE REPEATS (APPROXIMATE)
                                           DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS, THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF SPERMATOZOA OR PROMOTING ADHESION TO THE OVIDUCTAL ISTHWUS. DOMAIN: THE VWED DOMAINS 2 AND 3 MAY MEDIATE COVALENT OLIGOMERIZATION (BY SIMILARITY TO HUMAN INTESTINAL MUCIN MUC2). SIMILARITY: CONTAINS 3.5 MAM DOMAINS. SIMILARITY: CONTAINS 4.5 VWED DOMAINS.
APICAL REGION OF THE SPERM HEAD (BY SIMILARITY).
TISSUE SPECIFICITY: IN TESTIS; PRIMARILY IN HAPLOID SPERMATIDS
DOMAIN: THE MAM DOMAINS PROBABLY MEDIATE SPERM ADHESION TO THE
ZONA PELLOCIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC...) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell adhesion; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MUCIN-LIKE DOMAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGF-LIKE.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             i 1.
M 2 (PARTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNOKMA ->
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED
                                                                                                                                                                                                                                                                                                MAM.
P_rich_extensn.
TIL.
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                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00629, MAM; 3.
Pfam; PF01826; TIL; 4.
Pfam; PF00345; TILa; 4.
Pfam; PF00304; vwd; 4.
PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                EMBL; AF053356; AAC78790.1; -.
                                                                                                                                                                                                                                                                                    InterPro; IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00137; MAM; 2.
SMART; SM00214; VWC, 1.
SMART; SM00011; VWC_def; 3.
SMART; SM00216; VWD; 3.
PROSITE; PS01186; EGF_2; 3.
PROSITE; PS00740; MAM 1: 1.
PROSITE; PS50060; MAM_2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein; Transmembrane; NON_TER 1
                                                                                                                                                                                                                                                                                                Interpro; IPR000998; MAM.
Interpro; IPR002965; P_rich_
Interpro; IPR002919; TIL.
Interpro; IPR003328; TILa.
Interpro; IPR001007; WWFC.
Interpro; IPR001846; Vwd.
                                                                                                                                                                                                                                                             U83191; AAC51208.1; -
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161
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NON_TER
SEQUENCE
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Score 555.5; DB 1; Length 2700; Pred. No. 2.3e-15;

10.8%; 32.6%;

Query Match Best Local Similarity

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PKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKET--A 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPHPSPTA-TGLAALVMSPHAPSTPMTSV---ILGTTTTSRSSTGMSCP-PNARYESCAC 966
                                                                                                                                                                                                                                         232 TPKEPAPTTPKKPAPTTPKEPAPTTPKEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKP 291
                                                                                                                                                                                                                                                             351
                                                                                                                                                                                                                                                                                                                                                                                  406
                                                                                                                                                                                                                                                                                                                                                                                                      456
                                                                                                  SAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTTPKEPASTTPKEPT-----PTTI 172
                                                                                                                               SVTTEKPT-----VPKEKPTIPTEKPTISTEK---PTIPSEKPNMPSEKPTIPSEKPTIL 539
                               PINPRPSLPPNSDTSKETSLTVNKETTVETKETTTNKQTSTDGKEKTTSAKETQSIEKT 117
                                                                                                                                                                      173 KSAPTTPKEPAPTTTKSAPTTPKEPAPTTTKEPAPTTPKEPAPTTTKEPA-PTTTKSAPT 231
                                                               PVKVLPELPPVSPVSS----TGPSETTGLTENPTISTK------KPTVSIEKP 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CV. XANTHI: TISSUE-Leaf;
MEDLINE=90128263; PubMed=2612909;
MEDLINE=90128263; PubMed=2612909;
MEDLINE=90128263; PubMed=2612909;
Reller B., Lamb C.J.;
Rspecific expression of a novel cell wall hydroxyproline-rich glycoprotein gene in lateral root initiation.";
Glocks Dev. 3:1639-164(61989).
THE MECHANICAL HAS A SPECIALIZED STRUCTURAL FUNCTION, POSSIBLY IN THE MECHANICAL PENETRATION OF THE CORTEX AND EPIDERMIS OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nicotiana tabacum (Common tobacco).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; eugsterids I; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                            292 APITPKEPAPITPKEPAPITIKEPSPITPKEPAPITIKSAPITIKEPAPITIKSAPITPK
                                                                                                                                                                                                                                                                                                                                 - PITPTE-KPIIPTEKPIISTEKPTIPTEK-PIISPEKLTIPTEKLTIPT---EKPTIPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1990 (Rel. 13, Last sequence update)
01-JAR-1992 (Rel. 21, Last annotation update)
EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).
107;
64; Mismatches 240; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX
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     Matches 199; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           629 PTTPKEPAPT 638
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P13983;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              24;
EXTENSINS CONTAIN A CHARACTERISTIC REPEAT OF THE PENTAPEPTIDE PRO(4). THE PROLINE RESIDUE IS HYDROXYLATED AND THEN
                                                                                                                                                                                                                                                                        H-A-P-P.
H-A-P-P.
2 X 7 AA TANDEM REPEATS OF T-H-R-H-A-P-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 AETTIK-GPALTIP--KEPIPIT----PKEPASTIPKE---PIPITIKSAPTIPKEPAP 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185 TTTKSAPTTPKEP-----APTTTKEPAPT---TPKEPAPTTTKBPAPTTTKSAPTTPKE 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHGHLPPSVGGPPPHRGHLPPSRGFNPPPSPVISPSHPPPSYGAPPPSHGPGHLPSHGQR 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAPTIPKKPAPT---IPKEPAPITPKEPTPTTPKEPAPTIK--EPAPTIPKEPAPTAPKK 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 AEATTOYGGYLPPPVTSQPPPSSIGLSPPSAPTTTPPSRGHVPSP---RHAPPRHAYPPP 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAPTTPKEPAPTTPKEPAPTTTKEPSPTTPK---EPAPTTTKSAPTTTKEPAPTTTKS--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            88;
                                                                                                                                                                                                                                                                                                                                               CONTAINS THE SER-PRO(4) REPEATS.

3 X APPROXIMATE TANDEM REPEATS.

641DD2278AB28524 CRC64;
                                                                                                                                                                          EMBL; X13885; CAA32090.1;
PIR; S06733; S06733.
Repeat; Cell Wall; Glycoprotein; Signal; Structural protein;
                                                                                                                                                                                                                                                                                                                                                                                                                        10.7%; Score 551; DB 1; Length 620; 27.2%; Pred. No. 1.1e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           304; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                             EXTENSIN.
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148
229
229
236
205
499
620 AA;
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              SER-PRO(4). T
GLYCOSYLATED.
                                                                                                                                                                                                                          Hydroxylation.
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SEQUENCE
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REPEAT
DOMAIN
REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OF AXONAL CALLBER.

PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTIONING OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), THE LEYELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION.

SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.

CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN IN POSITIONS 534

TO 716 AND IS SHORFER DUE TO FRAMESHIFTS.
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDINE-89089138; PubMed-3145094;
Shheidman P.S., Carden M.J., Lees J.F., Lazzarini R.A.;
Shricture of the largest murine neurofilament protein (NF-H) as revealed by cDNA and genomic sequences.";
Brain Res. 464:217-231(1988).
                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                   Julien J.-P., Cote F., Beaudet L., Sidky M., Flavell D., Grosveld
                                                                                                                                                                                                                                                                                                                              "Sequence and structure of the mouse gene coding for the largest neurofilament subunit.";
Gene 68:307-314(1988).
                                                                                NFH_MOUSE STANDARD; PRT; 1087 AA.
P19246; Q61959;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 23, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN)
||| :| : |
---PTTYSPPSPPP 612
                                                                                                                                                                                                                                                                                       PubMed=3220257;
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EMBL; M23349; AAA39813.1;
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EMBL; M24495; AAA39813.1;
EMBL; M35131; AAA39809.1;
EMBL; Z31012; CAA83229.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA39813.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A43778; A43778.
MGD; MGI:97309; Nfh.
InterPro; IPR001664; IF.
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE-89121513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JT0368; QFMSH.
A43778; A43778
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                                                                                                                                                                                                                                                                                                                  Mushynski W.;
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 PSP-
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             599
                                                                    NFH_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP-APTITKEPAPTIPKEPAPTITKEP----APTITKSAPTIPKEPA----PTIPKKPA- 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGEAKSPAEPKSPAEA--KSPA----EVKSPAEAKSPAEVKSPGEAKS-PAAVKSPAEAK 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     343 IKSAPTIPKE-PSPTTKEPA----PTTPKEPAPTIPKKPAPTTPKEPAPTTPKEPAPTT 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   730 SPAAVKSPGEAKSPGEAKSPAEAKSPAEAKSPIEVKSPEKAKTPVKEGAKSPAEAKSPEK 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEP 457
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                                                                                                                                                                                                             OF K-S-P-A-E-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          790 AKSPVKEDIKPPAEAKSPEKA-KSPVKEGAKPPEKAKPLDVKSPEAQTPVQEEATVPTDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPKSPAEAKSPA--EPKSPA--TVKSPGEAKSPSEAKS-PAEAKSPAEAKSPAE
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Pfam; PF00038: filament; 1.
PROSITE; PS00226; IF; 1.
Intermediate filament; Coiled coil; Neurone; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 533; DB 1; Length 1087;
Pred. No. 8.7e-15;
1; Mismatches 330; Indels 158
                                                                                                                                                                                                                                                                                   LINKER 1.

COIL 1B.

LINKER 12.

COIL 2A.

LINKER 2.

COIL 2B.

K -> QA (IN REF. 2 AND 3).

S -> T (IN REF. 2 AND 3).

L -> G (IN REF. 2 AND 3).

P -> PREMSP (IN REF. 3 AND 3).

P -> A (IN REF. 2 AND 3).

G -> A (IN REF. 3).

MISSING (IN REF. 3).

MISSING (IN REF. 3).

T -> N (IN REF. 3 AND 3).

T -> N (IN REF. 2 AND 3).
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                                                                                                                                                                                  GLU-RICH (ACIDIC).
50 X 6 AA TANDEM REPEATS
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COIL 1A.
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27.5%;
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Matches 216; Conservative
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133
199
281
492
551
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240
2262
2262
2284
133
1199
1199
1281
551
689
6714
814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- DEVELOPMENTAL STAGE: MAXIMAL ACTIVITY IN TRYPOMASTIGOTES, MINIMUM IN EPIMASTIGOTES AND NO DETECTABLE IN AMASTIGOTES.
-!- MISCELLANDOUS: THE VARIABLE LENGTHS OF THE LONG TANDEM REPEAT DOMAIN COULD ACCOUNT IN PART FOR THE POLYMORPHISM OF THE TNCA
                                                                                                                                                                                               ---pk-meakvkeddkslskep--skpktekaekssstdokesoppe-----kttedka 1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The Trypanosoma cruzi neuraminidase contains sequences similar to bacterial neuraminidases, YWTD repeats of the low density lipoprotein receptor, and type III modules of fibronectin.";
                                                                                                                                                              743
                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
SIALIDASE (EC 3.2.1.18) (NEURAMINIDASE) (NA) (MAJOR SURFACE ANTIGEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      trypomastigotes.";
Trop. Med. Parasitol. 42:146-150(1991).
Trop. Med. Parasitol. 42:146-150(1991).
Trop. Med. Parasitol. 6 CELLS.
-!- FUKCTION: DEVELOPMENTALLY REGULATED NEURAMINIDASE IMPLICATED IN PARASITE INVASION OF CELLS.
-!- CATALYTIC ACTIVITY: HYDROLYSIS OF 2,3-, 2,6- AND 2,8-GLYCOSIDIC LINKAGES JOINING TERMINAL NON-REDUCING N- OR O-ACYLMEDIRANINYL RESIDUES IN OLIGOSACCHARIDES, GLYCOPROFEINS, GLYCOLIPIDS OR COLOMINIC ACID.
-!- SIBCELLIGAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-91375547; PubMed-1896773;
Prioli R.P., Mejia J.S., Aji T., Aikawa M., Pereira M.E.A.;
"Trypanosoma cruzi: localization of neuraminidase on the surface
564 KEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPTT
                                                                                                     | :| || :| |:|
-----KDTKEEKTTESRKPEEK-----
                                                                                                                                                            684 EPTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETA
                                                                              624 PKETAPITPKEPAPTIPKKPAPTTPETPPPTISEVSTPTITKEPTTIHKSPDESTPELSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-SILVIO X-10/4;
MEDLINE-91277609; PubMed-1711561;
Pereira M.E.A., Mejia J.S., Ortega-Barria E., Matzilevich D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO FAMILY 33 OF GLYCOSYL HYDROLASES. SIMILARITY: CONTAINS 3 BNR REPEATS.
                                          965 ETPAKLGVKEEA--KPKEKTETTKTEAEDTKAKEPS----KPTETEKP-----
                                                                                                                                                                                                                                                                                                                                                                                       1162 AA.
                                                                                                                              -----KKEEMPAAPEK------
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Eukaryota; Euglend
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                                                                                                                                                                                                                                                                                          1083 TKGEK 1087
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                                                   Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 APTSKVLAKP-TPK---AETTTKGPALTTPKEPTPTTPKEPASTTPKEPTFTKSAPTT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 VIIPAPAPIAAASVIPVASVAPPVVAAPIP-----PAASPVSTPVAVAQIPVAVSAPVAP 116
                                                                                                                                                                                                                                                                                         STRAIN—CANTON-S;

MEDLINE—93165730; Pubmed—8434015;

MEDLINE—93165730; Pubmed—10, Pubmed—
                                                                                                                                                                                                                                                                                                                                                         calphotin, binds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234 KEPAPITPKKPAP-----TTPKEPAPTTPKEPTP-----TTPKEPAPTTKEPAPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 SPVSAPVAAPVTPSAVAAPVQVVSPAAVAP-----APAAPIAVTPVAPPPTLASVQPAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PKEPAPTTTKSAPTTP-KEPAPTTKEPAPTTPKEPAPTTTKEPAPT----TTKSAPTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      433; Indels 152;
                                                                                                                                                                    STRAIN-CANTON-S;
MEDLINE-93165729; PubMed-8094559;
Martin J.H., Benzer S., Rudnicka M., Miller C.A.;
"Calphotin: a Drosophila photoreceptor cell calcium-binding Proc. Natl. Acad. Sci. U.S.A. 90:1531-1535(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; DB 1; Length 865; 9.5e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A -> AVAPAVVA (IN REF. 2).
I -> T (IN REF. 2).
I -> V (IN REF. 2).
T -> A (IN REF. 2).
VQ -> PP (IN REF. 2).
VQ -> PP (IN REF. 2).
I -> V (IN REF. 2).
I -> V (IN REF. 2).
I -> T (IN REF. 2).
S -> T (IN REF. 2).
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I -> T (IN REF. 2).
I -> T (IN REF. 2).
D -> E (IN REF. 2).
W; 2110417E0B067CFE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 530;
Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Σ.
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26.2%;
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FlyBase; FBgn0010218; Cpn.
Calcium-binding.
CONFLICT 36 36
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865 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEPTP-TIPKEPAPTIKEPAPTTPKEPAPTAPKKPAPTTPKEPAPTTPKEPAPTTTKEPS 316
                                                                                                                                                                                                                                                                                                                                                                                      711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TP-KKPAPTTPKEPAPTTPKEPAPTTTKKPAPTAPKEPAPTTPKETAPTTPKKL----TP 427
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                                                                                                                                                         TERRONECTIN TYPE-III.

44 X 12 AA TANDEM REPEATS, LTR DOMAI
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
Wr. 07049221897C6A40 CRC64;
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                                                                                                                                                                                                                                                                                                           Length 1162;
                                                              Repeat; GPI-anchor;
                                                                                                                                                                                                                                                                                              Query Match
10.3%; Score 530.5; DB 1;
Best Local Similarity 29.4%; Pred. No. 1.1e-14;
Matches 177; Conservative 100; Mismatches 212;
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(Rel. 27, Last sequence update)
(Rel. 28, Last annotation update)
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HSSP; P29768; IDIL.
InterPro; IPR002860; BNR.
Pfam; PF02012; BNR; 2.
Hydrolase; Glycogldase; Glycoprotein;
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Q02910;
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CPN_DROME
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414 V----LPPVAAEPVPAVVAEETPETPAPASAPVTIAALDIPEVAPVIAAPSDAPAEAPSA 469
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90-MAY-2000 (Rel. 39, Last sequence update)
10-AUG-2001 (Rel. 40, Last annotation update)
ADHESIVE PLAQUE MATRIX PROTEIN PRECURSOR (FOOT PROTEIN 1) (MCFP1).
                                                                                                                                                                                                                       TPEKL-APTTPEKPAPTTPEELAPTTPEEPTPTTPEEP---APTTPKAAAPNTPKEPAPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    740 KETATTTEKTTESKITATTTQVTST-----TTQDTTPFKITTLKTTTLA-PKVTTTKKT
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                                                                                                                                                                                                                                                                                                                                             534 LAPTITKEPISTISDKPAPTIPKGTAPTIP-----KEPAPTIPKEP--APTIPKGTAPI
                                                                                                                                                                                                                                                                                                                                                                        470 AAPIVSTPP--TTASVPETTAPPAAVPTEPIDVSVLSEAAIETPVAPPVEVTTEVAVADV
                                                                                                                                                                                                                                                                                                                                                                                                       586 TLKEPA-----PTTPKKPAPKELAPTTT----KGPTSTTSDKPAPTT----PKETAPTT
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Eukaryota, Mettazoa, Mollusca: Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilus.
NCBI_TaxID=42192;
                                                                     AAVPAAVPVVAPVLAPAVAPAVAPVVAETPAPPPVAEIPVATIPECVAPLIPEVSVVATK
                                                                                                     --APTTTKSAPTTPKEPSPTTTKEPA-PTTPKEPAPTTPKKPAPTTPKEPAP
                                                                                                                        PKEPA--PTAPKKPAPTTPKEPAPTTPKEPAPTTKE-PSPTTPKEPAP-----TTTKSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          853 PRKMTSTMPELNPTSRIAEAM---LQTTTRPNQTPNSKLVEVN-----PKS:895
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Inoue K., Takeuchi Y., Takeyama S., Yamaha E., Yamazaki F.,
Harayama S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LRDLQTTDVSLLAIAATLDAIGEKLKDQKARNQQVMDRLCEIEKILGPPKS 864
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                                                                                                                                                                 TTP------REPAPTTTKKPAPTAPKEP----APTTPKET-
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Q25434;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MOI. EVOI. 43:348-356(1996).
FUNCTION: PROVIDES ADHESIVENESS TO THE MUSSEL'S FOOT. MUSSELS PRODUCE ONE OF THE STRONGEST WATER INSOLUBLE GLUE. THE MUSSEL'S PRODUCE ONE OF THE STRONGEST WATER INSOLUBLE GLUE. THE MUSSEL'S ADHESIVE IS A BUNDLE OF THREADS, CALLED A BYSSUS, FORMED BY A FIRROUS COLLAGENOUS CORE COAPED WITH ADHESIVE PROTEINS. SUBCELLUILAR LOCATION: SECRETED.
TISSUE SPECIFICITY: PRODUCED BY THE BYSSAL GLAND.
DOMAIN: ALMOST EXCLUSIVELY COMPOSED OF REPEATS OF A DECAPEPTIDE.
PTM: PROLINES IN THE REPEAT ARE HYDROXYLATED (SINGLE OR DI-) AND ALSO TYROSINE (THUS PRODUCING DOPA = 3,4-DIHYDROXYPHENYLALANINE).
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NONAPPORT
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Pred. No. 2.7e-14;
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Interpro; IPR002964; Adhesive_plaq.
Interpro; IPR002965; P_rich_extensn.
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PRINTS; PR01217; PRICHEXTENSN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hauser F., Hoffmann W.;

T. T. Grim-C.1) from Xenopus laevis. Polydispersity and genetic

C.1 (FIM-C.1) from Xenopus laevis. Polydispersity and genetic

C.1 (FIM-C.1) from Xenopus laevis. Polydispersity and genetic

G.1 (FIM-C.1) from Xenopus laevis. Polydispersity and genetic

G.1 (FIM-C.1) from Xenopus laevis. Polydispersity and genetic

G.1 - FUNCTIONS. COULD BE INVOLVED IN DEFENSE AGAINST MICROBIAL

INFECTIONS. PROTECTS THE EPITHELIA FROM EXTERNAT L.

G.1 - ALTERNATIVE PRODUCTS: A NUMBER OF DIFFERENT FORMS OF THE PROTEIN

MAY BE PRODUCED BY ALTERNATIVE SPLICING.

G.1 - ALTERNATIVE SKIN.

C.1 - TISSUE SPECIFICITY: SKIN.

C.1 - FIM: EXTENSIVELY O-GIYCOSYLATED.

C.1 - PTM: EXTENSIVELY O-GIYCOSYLATED.
470 PTYKPKPSYPPTYKPKITYPPTYKRKPSYPTPYKQKPSYPPIYKSKSSYPTSYKSKKTYP 529
                       TT--PKGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKPAPT-TPKGTAPTTPK 564
                                                                                                                                                                670 IHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKT----TERDL 725
                                                                                                                                                                                RTTPETTTAAPKMIKETATTTEKTTESKITATTTQVTSTTTQDTTPFKITTLKTTTLAPK 785
                                                                                                                                                                                                                              786 VITTKKIITTEIMNKPEETAKPKDRAINSKAITPKPQ---KPTKAPKKP-TSTKKPK-T 840
                                                                                                                                                                                                                                                                             530 PTYKPKITYPPTYK-----PKPSYPPSYKPKTTYPPTYKPKIRYPPTYKPKASYPPTYK
                                                                     EPAPTTPKEPAPTTPKGTAPTTLKEPAPTTP----KKPAPKELAPTTTKGPTSTTSDKPA
                                                                                   PTT--PKETAPTTPKEPAPTTPK--KPAPTTPET-----PPPTTSEVSTPTTTKEPTT
                                                                                                                                                                                                                                                                                                                                                                                                               OLOCT-1994 (Rel. 30, Last sequence update)
01-OCT-1994 (Rel. 30, Last sequence update)
10-OCT-1994 (Rel. 30, Last annotation update)
INTEGUMENTARY MUCIN C.1 (FIN-C.1) (FRAGMENT).
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                          841 MPRVRKPKTT--PTPRKMTSTMPELNPTSRIAEAMLQTTTRPNQ 882
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HSSP; P04002; 1WFA.
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P-TYPE 1.
8 X APPROXIMATE TANDEM REPEATS, THR-RICH.
2-1.
                                              8 AA APPROXIMATE TANDEM REPEATS,
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P-TYPE 3.
12 X APPROXIMATE TANDEM REPEATS,
THR-RICH.
Pfam; PF00088; Lefoil.
Pfam; PF00088; P. Lrefoil; 6.
SWART; SM00018; P. 6.
PROSITE; PS00025; P_TREFOIL; 6.
Repeat; Amphibian skin; Glycoprotein; Alternative splicing.
NON_TER 81 144
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P-TYPE 5.
P-TYPE 6.
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Query Match 9.9%; Score 509.5; DB 1; Length 662; Best Local Similarity 28.1%; Pred. No. 4.9e-14; Matches 223; Conservative 48; Mismatches 276; Indels 247; Gaps

30;

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604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 665 KEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPTIKTPAATKPEMTTTAKDKTTERD 724
                                                                                                                                                                                                                                                           PSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKEPAPTTPKEPAPTTP 374
                                                                                                                                                                                                                                                                                                                          375 KKPAPTTPKEPAPTTPKEPAPTTKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEKLA 434
                                                                                            ------AAATAAAETTAAAGEAPTTTTAPATTAAGKAPTTAAATAPTTAAAGAPTTAT 103
TINKQISIDGKEKTISAKETQSIEKTSAKDLAPISKVLAKPIPKAETTIKGPALTIPKEP 151
                              51
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20-AUG-2001 (Rel. 40, Last annotation update)
DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      785 KVTTTKKTITTTEIMNKPEETAKPKDRAINSKATTPKPQKPTKAPKKPTSTKKPK----T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              511 TITITKATITITSGECKME----PSKRADCGYPGITESQCRSKGCCFDSSIPQTKWCFYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      495 KEPAPITPKETAPITPKGTAPITLKEPAPITPKKPAPKELAPITIKEPISITSDKPAPIT
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                                                                                                                                                           104 GKAPATAAAPVPTTAASKAPTTAAAATHSTAAAAPTTAASAAKSKERSTSSSSEEEHCH
                                                                                                                                                                                                                  164 VKPSKREMCGSKGIIKKQ----CKKKNCCFDPKGHGGIHCFHRKPKGHSHEEHTTTTK-
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                            EPAPTTTKEPAPTTTKS-APTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPTTPKEPA-
                                                                                                                                                                                             --PITKEPAPT---TPKEPAPTAPKKPAPTTPK------EPAPTTPKEPAPTTKE
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SEQUENCE FROM N.A.
MEDLINE=92178992; PubMed=1542581;
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(Rel. 21, Last seq
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567 LPQVADCKVAPSSR 580
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P24928;
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01-MAR-1992 (
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Wintzerith M., Acker J., Vicaire S., Vigneron M., Kedinger C.; "Complete sequence of the human RNA polymerase II largest subunit."; Nucleic Acids Res. 20:910-910(1992).
                                                                                                                                                                                                            RNA(N):
SUBUNIT: RNA POLYMERASE II CONSISTS OF 12 DIFFERENT SUBUNITS.
SUBUNIT: ALCATION: NUCLEAR.

PTM: THE TANDEM 7 RESIDUES REPEATS CAN BE HIGHLY PHOSPHORYLATED.
THE PHOSPHORYLATION ACTIVATES POLZ.
MISCELLANEOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES ARE FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE III FOR SA AND TRNA GENES.
SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
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ilarity 33.3%; Pred. No. 2e-13;
Conservative 101; Mismatches 167;
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EMBL, X74874, CAA52862.1; --
EMBL, X74873, CAA52862.1; --
EMBL, X74873, CAA52862.1; JOINED.
EMBL, X74871, CAA52862.1; JOINED.
EMBL, X74870, CAA52862.1; JOINED.
PIRE, X21054, S21054.
MIN; 180660; --
INTEPTPO; IPRO00722; RNA_POL_A.
INTEPTPO; IPRO0229; RNA_POL_A.
INTEPTPO; IPRO0229; RNA_POL_A.
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Matches 181; Conserv
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SEQUENCE FROM N.A.
MEDLINE-87280135; PubMed-3038894;
MEDLINE-87280135; PubMed-3038894;
Ahearn J.M. Jr., Bartolomei M.S., West M.L., Cisek L.J., Corden J.L.;
"Cloning and sequence analysis of the mouse genomic locus encoding the largest subunit of RNA polymerase II.";
J. Biol. Chem. 262:10695-10705(1987).
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-1- SUBCELLULAR LOCATION: NUCLEAR.
-1- PTM: THE TANDEM 7 RESIDUES REPEATS CAN BE HIGHLY PHOSPHORYLATED.
THE PHOSPHORYLATION ACTIVATES POLZ.
-1- MISCELLANBOUS: THRRE DISCTINCT ZING-CONTAINING RNA POLYMERASES ARE FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA PRECURSOR, POLYMERASE IT FOR THE MRNA PRECURSOR, AND POLYMERASE
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MEDLINE-86068017; Pubmed-2999785;
Corden J.L., Cadena D.L., Ahearn J.M. Jr., Dahmus M.E.;
"A unique structure at the carboxyl terminus of the largest subunit of eukaryotic RNA polymerase TT".
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-1- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE
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01-MAR-1992 (Rel. 21, Last Sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1).
POLRZA OR RPO2-1 OR RPI1215.
                                                             KEPAPTTPKEPAPTTKKPAPTAPKEPAPTTPKETAPTTPKKLJPTTPEKLAPTTPEKPA
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Sciurognathi; Muridae; Murinae; Mus
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Proc. Natl. Acad. Sci. U.S.A. 82:7934-7938(1985).
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Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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III FOR 55 AND TRNA GENES.
SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:| :||: ||:| :||:| | :||:| | :||:| | ||:| | ||:| | ||:| | ||:| | ||:| | ||:| | ||:| | ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
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9.7%; Score 498.5; DB 1;
Best Local Similarity 33.1%; Pred. No. 3.1e-13;
Matches 180; Conservative 101; Mismatches 168;
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PIR; A28490; A28490.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M12130; AAA40071.1;
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PPOC. Natl. Acad. Sci. U.S.A. 86:2467(1989).

- !- FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M, AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER.

NP-H HAS AN IMPORTANT FUNCTION IN MATURE AXONS THAT IS NOT SUBSERVED BY THE TWO SMALLER NF PROTEINS.

- !- PTM: THERE ARE A NUMBER OF THE SERINES IN THIS MOTIF. IT IS PHOUGHT THAT PHOSPHORYLATION OF NEH RESULTS IN THE FORMATION OF THOUGHT THAT PHOSPHORYLATION OF NEH RESULTS IN THE MAINTENANCE OF AXONAL CALIBER.

- !- PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE MAINTENANCE OF THE LARGER NEUROFILAMENT FOLYBETINGS (NF-M AND NF-H), THE CONTICIONING COUNCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE INTERNEDIATE FILAMENT FAMILY.
CAUTION: REF.1 SEQUENCE DIFFERS FROM THAI SHOWN FROM POSITION 783
ONWARD AND IS LONGER DUE TO A FRAMESHIFT.
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                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                        The large neurofilament subunit (NF-H) of the rat: cDNA cloning and
                                                                                                                                                                                                                                                                                                               Breen K.C., Robinson P.A., Wion D., Anderton B.H.; "Partial sequence of the rat heavy neurofillament polypeptide (NF-H). Identification of putative phosphorylation sites.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-89184647; PubMed-2928342; Anderson J., Goldgaber D., Liberburg I., Spinner N., Snyder S., Anderson J., Goldgaber D., Smulowitz M., Carroll Z., Emanuel B.S., Breitner J., Rubin L.; "Cloning of a cDNA encoding the rat high molecular weight neurofilament peptide (NF-H): developmental and tissue expression the rat, and mapping of its human homologue to chromosomes I and 22.";
                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-88309090; PubMed=2457365;
Dautigny A., Pham-Dinh D., Roussel C., Felix J.M., Nussbaum J.L., Jolles P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Robinson P.A., Wion D., Anderton B.H.; "Isolation of a cDNA for the rat heavy neurofilament polypeptide
                                                                                                           01-FEB-1994 (Rel. 28, Last sequence update)
20-AGG-2001 (Rel. 40, Last annotation update)
NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN)
(NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H) (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. Biophys. Res. Commun. 154:1099-1106(1988)
                                                                 831 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-89 AND 243-313 FROM N.A.
MEDLINE-87080760; Pubmed-2878828;
                                                                   PRT;
                                                                                                                                                                                                                                                                                           TISSUE=Brain;
MEDLINE=89065087; PubMed=3143606;
                                                                                                 01-AUG-1990 (Rel. 15, Created)
01-FEB-1994 (Rel. 28, Last seq
                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EBS Lett. 209:203-205(1986).
                                                                                                                                                                                                                                                                                                                                                                  FEBS Lett. 241:213-218(1988)
                                                                   STANDARD;
                                                                                                                                                                                             Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in situ detection.
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                    063368;
                                                                                                                                                                                  NEFH OR NFH
                                                                     NFH_RAT
P16884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NF-H)
                                       15
                                                         NFH RAT
                                         RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97 ISTDGKEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEP----T 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                245
                                                                                                                                                                              intermediate filament; Coiled coil; Neurone; Phosphorylation; Repeat.
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L -> 5 (IN REF. 2).
L -> T (IN REF. 2).
M -> T (IN REF. 2).
K -> N (IN REF. 1).
K -> N (IN REF. 1).
G -> E (IN REF. 2 AND 4).
P -> S (IN REF. 2 AND 4).
RK -> KE (IN REF. 2 AND 4).
P -> T (IN REF. 2 AND 4).
R -> T (IN REF. 2 AND 4).
A -> V (IN REF. 4).
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-> P (IN REF. 2 AND 4).
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Best Local Similarity 27.6%; Pred. No. 1.8e-13;
Matches 195; Conservative 59; Mismatches 307
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T -> L
EMBL; X13804; CAA3203.1; ALT_FRAME.
EMBL; X13804; CAA32038.1; ALT_FRAME.
EMBL; M21964; AAA41695.1;
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Pfam; PF00038; filament; 1.
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                                                    J04517; AAA41692.1;
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727
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769
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185
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346
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PIR; A25649; A25649.
PIR; B25649; B25649.
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701 KKEEAKEKKAAAPEEETPAKLGVKEEAKPKEKAEDAKA 570 TPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSI :	IGVKEEARPKEKAEDAKAKEPSKP 744	570 TPKEPAPITPKGTAPITLKEPAPITPKKPAPKELAPITIKGPISTISDKPAPITPKETAP 629	745 SEKEKPKKEEVPAAPEKKDTKEEKTTESKKREEKPKMEAK 784	TTSEVSTPTTTKEPTTIHKSPDE 676	: : : EKAEKSSSTDQKDSQPSEKAPED 824
	701 KKEEAKEKKAAAPEEETPAKLGVKEEAKPKEKAEDAKA	570 TPKEPAPTTPKGTAPTTLKEPAPT	745 SEKEKPKKEEVPA	630 ТТРКЕРАРТТРККРАРТТРЕТРРРТТЅЕVSTРТТТКЕРТТІНКЅРDE 676	785 AKEEDKGLPQEPSKPKTEKAEKSSSTDQKDSQPSEKAPED 824

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ORIGINAL SOURCE
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Sequence 6, Appli
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Sequence 2, Appli
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Sequence 23, Appli
Sequence 132, Appli
Sequence 132, Appli
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Sequence 133, Appli
Sequence 133, Appli
Sequence 134, Appli
Sequence 101, Appli
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                                                                          US-09-556-246-1_COPY_200_1167
5155
1 VKDNKKNRTKKKPTPKPPVV.....GKPVDGLTTLRNGTLVAFRG
                                             ; Search time 49.78 Seconds
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/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/PcTUS_COMB.pep:*
  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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US-07-609-716-65
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                                                                                                                               212252 seqs, 22503292 residues
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Maximum Match 100%
Listing first 45 summaries
                             OM protein - protein search, using sw model
                                             April 26, 2002, 16:16:52
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Gapop 10.0 , Gapext 0.5
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Match 1
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Perfect score:
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Score 522; DB 4; Pred. No. 5.2e-26;

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                                                                                      ------EPAPTITK 399
                      TSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAP----TTP 179
                                                                        KEPAPTT-----TKSAPTTPKEPAPTTTKEPAPTTPKEPAPTTTKEPAPTTTK 227
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 342;
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; Patent No. 5202236
; APPLICANT: MAUCH, KATHY J.; ANDERSON, DAVID
; SUSAN L.; MCCANDLISS, RUSS; WEL, TENA; FILPULA, DAVID
; TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
  Indels
  211;
    Mismatches
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/07/528,762
FILING DATE: 25-MAY-1990
APPLICATION NUMBER: 82,456
FILING DATE: 07-AUG-1987
APPLICATION NUMBER: 933,945
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     226; Conservative
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                                                                                                                                               PKITTAKPINPRPSLPPNSDTSKETSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          602 YKAKPSYPPTYKAKPSYPPTYKAKPSYPPTYKAKPTYPSTYRAK
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                                                                                                                                                                                                                                                                                                                                                                                                                  378 A--PITPKEPA--PITPKEPA--PITIKKPA--PIAPKEPAPITPKETAPITPKKLIPIT
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                                                                                                                                                                      24 PKMTYPPTYKPKPSYPP-----TYKSKPTY------KPKIT----
                                                                                                                         Indels 175;
                                                                                                 Length 744;
                                                                                               9.8%; Score 506.5; DB 6;
29.9%; Pred. No. 4.6e-25;
ive 78; Mismatches 308;
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US-08-928-361B-5
; Sequence 5, Application US/08928361B
; Patent No. 6071518
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; FILING DATE: 24-NOV-1986
; APPLICATION NUMBR: 650,128
; FILING DATE: 13-SEP-1984
; SEQ ID NO:25:
LENGTH: 744
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                                                                                                                             Conservative
                                                                                                                 Similarity
                                                                                                                              Matches 239;
                                                                                                      Query Match
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1016 PP---EVAAANADKFKLSIPPSVPESIPEKDQKIDSISELMYDIESGRLIGOVSKRPIPG 1072
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                                                                                                                          TPKEPAPTTTKKPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEE 448
                                                                                                                                                            678 ISADFVTTTTAKPTTTT--TGAPGQPTTTTTGSPSKPTTTTTKATTTT-----TILNP 729
                                                                                                                                                                                                                                    730 IITTTTQKPTTT-----T----KVPGKPPIATTTTLKPIVTTTTKATTTTTVPT 780
                                                                                                                                                                                                                                                                                                                                                                                         836 PIPGSQAGQIADTSNLFPVQTHKSTGLPIDPMVGLPFDPKSGNLVHPYTNQTMSGLSVSY 895
            KDGRIENGMAFTMIPNDDTHVRFRFKVKDVGNTISVRCGKGAGKLEFPDRSLDFTIPPVA 617
                                                                                                                                                                                                                                                                                      ---TTSDK 549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Granados, Robert R
APPLICANT: Wang, Ping
TITLE OF INVENTION: A No. 6187558el Invertebrate Intestinal Mucin
TITLE OF INVENTION: c.DNA and Related Products and Methods
                                                                                                                                                                                                  LAPTTPEEPTPTTPEEPAPTTPKAAAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPT
                                                                                                                                                                                                                                                                                                    896 LAAKNLIVDIDEIYGLPIDILIGYPLDPVSLIPFNPETGELFDPISDEIMNGIIAGIVSG
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Pinnisi & Michaels, P.C.
STREET: 118 No. 6187558th Tioga
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US-09-103-429A-3
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                  , Carolyn PEPTIDES, GLYCOPROTEINS, THEIR FUNCTIONAL MUTANTS, VARTANTS, ANALOGS AND FRAGMENTS FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM SPECIES INFECTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----EKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTPKE 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAPCNSENSFEQVQIFDMGSKVYIPYTKCVGVKHTTTTTTT----TTTTTTTTTT 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 279 TPKEPAPTAPKKPAPTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKEP 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGLPTDPYPNCPFNPVTGNLVSRSTGKTIPNTYAGVYRSNETKTTEPSANTNFLLVDPKI 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          443
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9.8%; Score 504; DB 3; Length 1837;
Best Local Similarity 22.3%; Pred. No. 1.8e-24;
Matches 279; Conservative 81; Mismatches 481; Indels 412; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PASTTPKEPTPTTIKSAPTTPKEPAPTTTKSAPTTPKEPAPTTTKEPAPTTPKEPAPTTT
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                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           339 APTITKSAPTIPKEPSPTITKEPAPTIPKEPAPTIPKK-
                                                                                                                                              SEE: PETERS, VERNY, JONES & BIKSA: 385 Sherman Avenue, Suite 6
Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     480.76-1(HV)
                                                                                                                                                                                                                                                                                                                                                                             UMBER: US/08/928,361B
12-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION:
TELEPHONE: 650-324-1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1837 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           650-324-1678
                                                                                                        NUMBER OF SEQUENCES: 3C
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: protein US-08-928-3618-5
                      Petersen,
                APPLICANT: Petersen,
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 94306-1840
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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                                                                                                                                                                  STREET:
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TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS TITLE OF INVENTION: INPECTIONS TITLE OF INVENTION: INFECTIONS FILE REFERENCE: 480.19-4(HV) CURRENT APPLICATION NUMBER: 08/710,651B CURRENT FILING DATE: 1997-08-14 EARLIER PAPLICATION NUMBER: 08/415,751 EARLIER FILING DATE: 1995-04-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---TSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAK 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 KKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRPS 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   290 KPAPTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170 TIIKSAPITPKEPAPITIKSAPTIPKEPAPITIKEPAPITPKEPAPITIKEPAPTITKSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  230 PTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPK
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PAPITPKETAPITPKGTAPITLKEPAPITPKKPAPKELAPITIKEPISITSDKPAPTIPK
                                                                                               633 TAAPTT-AAPAPNTTVTVPPTAAPTAAPPTVAH-------APNTTAAPVTTTS
                                                                  GTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.5%; Score 489; DB 3; Length 1721;
22.1%; Pred. No. 1.5e-23;
.ive 82; Mismatches 476; Indels 442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              588 AAPTAAPTTAVPEIPTTVTSPPTAAPTTAAP---APNTT-
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                                                                                                                                         617 DKPAPTTPKETAPTTPKEPAPTTPKKP 643
                                                                                                                                                                  ---APATTPEDDDIDP--PLPNDPINP 699
                                                                                                                                                                                                                                                           Sequence 5, Application US/08700651B Patent No. 6015882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT; ORGANISM: Cryptosporidium parvum
US-08-700-651-5
                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLYN
APPLICANT: LEECH, JAMES
APPLICANT: NELSON, RICHARD, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patentin Ver. 2.0
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Matches 284; Conserv
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US-08-700-651-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 ELLPNGCPADFDIHLLIPHDKYCNLFYQCSNGYTFEORCPEGLYFNPYVORCDSPANVEC 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302 DGEISPAPPVTEGNEDEDIDIGDLLDNGCPANFEIDWLLPHGNRCDKYYQCVHGNLVERR 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAPTTPKEPAPTTKSAP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTPKEPAPITIKEPAPITPKEPAPITIKEPAPITIKSAPITPKEPAPITPKKPAPITPKE 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421 ADFSIDHLLPHESDCGQYLQCVHGQTIARPCPGNLHFSPATQSCESPVTAGCQVFECDSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----APTTPKKPAPTT
                                                               COMPUTER: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/09/103,429A
FILING DATE: 24-JUN-1998
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.7%; Score 498.5; DB 4;
29.1%; Pred. No. 1.6e-24;
tive 25; Mismatches 207;
                                                                                                                                                                FILING DATE: 4-100
CLASSIFICATION: 800
ATTORNEY AGENT INRORMATION:
NAME: Michaels, Christopher A
REGISTRATION NUMBER: 34,390
REFERENCE/DOCKET NUMBER: BTI-39
TELECOMMUNICATION: TELECOMMUNICATION:
TELEPHONE: (607) 256-300
TELEFAX: (607) 256-300
TELEFAX: (607) 256-3628
; INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
: ACRUTH: 786 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , ORGANISM: Trichoplusia ni
;
US-09-103-429A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 29.15
Matches 200; Conservative
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                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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ORIGINAL SOURCE:
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                   COUNTRY:
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41;

STREET: 385 Sherman Avenue, Suite 6 CITY: Palo Alto STATE: CA COUNTRY: USA ZOWTRY: USA ZIP: 94306-1840 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: TBM PC Compatible OPERATING SYSTEM: PC-DCS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/928,361B FILING DATE: 12-SEP-1997 CLASSIFICATION: PRIOR APPLICATION DATA: APPLICATION NUMBER: US 60/026,062 FILING DATE: 13-SEP-1996 ATTORNEY/AGENT INPORMATION: NAME: Verny, Hana REFERENCE/DOCKET NUMBER: 30,518 TELECOMMUNICATION INFORMATION: TELECHONE: 6560-324-1677 TELECHONE: 6560-324-1677	D 20.2471678 D 20.2471678 D 20.267 D 21 amino acids D 22 acid D 22 18; Score 489; DB 3; Length 1721; D 3 2 18; Pred. No. 1.5e-23; Conservative 82; Mismatches 476; Indels 442; Garannian	11 15 11 11 17 17 24:	TTTTATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
467 369 411 471 471 628 531 581 741 741	ALIDPA LENSPK : KLSIP- TAAPKM AGDLNP TITTTE	RREP VNNP DTTC TINTC PRVIE PRVIE PRVIE I I I I I I I I I I	RESULT 6 US-08-928-361B-6 US-08-928-361B-6 Sequence 6, Application US/08928361B Patent No. 6071518 GENERAL INFORMATION: GENERAL INFORMATION: TITLE OF INVENTION: CORRESPONDENCES: 30 CORRESPONDENCE ADDRESS: ADDRESSEE: PETERS, VERNY, JONES & BIKSA

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1084 NLFDPSTNLPIDGNNQLVNPETNSTVSGSTSGTTKPKPGIPVNGGGVVPDEEAKDQADKG 1143
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APPLICANT: Hoffman, Stephen L.
APPLICANT: Hedstrom, Richard
APPLICANT: Hedstrom, Richard
APPLICANT: Rogers IV, William O.
TITLE OF INVENTION: Immunogen and gene
TITLE OF INVENTION: Immunogen and gene
NUMBER OF SEQUENCES:
CORRESEDED ADDRESS:
ADDRESSEE: A David Spevack
STREET: Medical Center
CITY: Bethesda
STATE: MD
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9.5%, Score 488.5; DB 1;
Best Local Similarity 26.4%; Pred. No. 7.2e-24;
Matches 153; Conservative 54; Mismatches 223;
          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/638,431
FILING DATE: 19910110
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                                                                                                                                      CLASSIFICATION: 424
ATTORREY/AGENT INFORMATION:
NAME: SPEVACK, ANTOM D.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 295-6759
TELEPHONE: (301) 295-6733
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHRARACTERISTICS:
LENGTH: 826 amino acids
TPPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: protein US-07-638-431-2
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20814-5044
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CLASSIFICATION:
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Best Local :
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 295-6759
TELEFAX: (301) 295-4033
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: Spevack, Avram D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: Immunogen and gene
   571
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les 153; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: A. David Spevack
STREET: NMRDC Building 1 T-12 National Naval
STREET: Medical Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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ZIP: 20814-5044
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PKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPT
                                                                                                                    KGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTT | : | | | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
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Khusmith, Srisin
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26.4%; Pred. No. 7.2e-24;
tive 54; Mismatches 223
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it, Yupin
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RESULT 9
5202236-13
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; APPLICANT: MAUGH, KATHY J.; ANDERSON, DAVID M.; STRAUSBERG, SUSAN L.; MCCANDLISS, RUSS; WEI, TENA; FILPULA, DAVID; TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE;
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                                        488 EPA-PTT----PKEPAPTTPKETAPTT--PKGTAPTTLKEPAPTTPKKPAPKELAPTTTK 540
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FILING DATE: 07-AUG-1987
APPLICATION NUMBER: 933,945
FILING DATE: 24 NOV-1986
APPLICATION NUMBER: 650,128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
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                                                                                AKPTYPSTYKAKPSYP----PTYKAKPSYPPTYKAKPSYPPTYK-AKPSYP----PTYKA 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTKSAPTTPKEPAPTTPKKPAPT-TPKEPAPTT----PKEPTPTTPKEPAPTTKEPAPT 278
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KPTYPSTYKAKPSYPPTYKPKISYPPTYKAKPSYPSTYKAKSSYPPTYKAKPSYPPTYKA 473
                                                                                                       LAPTTPE--KPAPTTPEELAPTTPEEPT--PTTPEEPA-PTTPKAAAPNTPKEPAPTTPK 487
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                                                                                                                                                                                                                                                                                                SAPTITKEPA----PTTTKSAPTTPKEPSPTTTKEPA--PTTPKEPA----PTTPKK 376
                                                                                                                                                                                                                                                                                                                                           YP----PTYKAKPSYPPTYKAKPSYPPTYKAKPSYPPTYKAKPSYPSLIKAKPSYPPTYK 252
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LENGTH: 960

TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Illustrative
OTHER INFORMATION: amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: WIND, RICHELE D.
APPLICANT: VAN DEN BOSCH, TANJA J.
TITLE OF INVENTION: SILVER HALIDE EMULSIONS WITH RECOMBINANT COLLAGEN
TITLE OF INVENTION: SUITABLE FOR PHOTOGRAPHIC APPLICATION AND SIGN TITLE OF INVENTION: PREPARATION THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/09219849 Patent No. 6150081
                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/219,849
CURRENT FILING DATE: 1998-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
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                                                                                                                                         187
                                                                                                                                                                                                             127
                                                                                                                                                                                                                                               190
                                                                                                                                                                                                                                                                                                                 132 PTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAPTTPKEPAP--TTTKS 189
                                                                                                                                                                            246
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                                                                                                                                                                                                             GPPGSRDPGPPGAPGPAGPPGSRDPGPPGAPGPPGSRDPGPPGAPGPAGPPGSRDPG 186
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GPPGSRDPGP----
                                APTTTKEPAPTTTKSAPTTPKEPSPTTTKEPAPTTPKEPAPTTP---KKPAPTTPKEPAP 387
                                                                                                                                                                            PTTPKEPAPTTP---KEPTPTTPKEPA--PTTKEPAPTTPKEPA-------
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                                                                                                                                                                                                                                                                                PGPAGPPGSRDPG--PPGAPGPAGP--PGSRDPGPPGAPG-PAGPPGSRDPGPPGAPGPA 126
                                                                     PAGPKGAHGPAGPKGAPGPAGPPGSRDPGPPGAPGPPGSRDPGP---PGAPGP----A
                                                                                                                                         P--PGAPGPAGPPGSRDPGPPGAPGPAGPPGSRDPGPPGAHGPAGPKGAHGPAGPKGAHG
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VAN RIJN, ALEXIS C.
BOUWSTRA, JAN B.
DE WOLF, FREDERIK A.
                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                    -PTAPK-KPAPTTP---KEPAPTTPKEPA-PTTTKEPSPTTPKEPAPTTTKS 330
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Pred. No. 1.8e-21;
50; Mismatches 309
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US-08-479-537A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION
                                                                                                                                                                                                                              CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: FR 90/13101
                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,537
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                  APPLICATION NUMBER: 1
FILING DATE: 23-OCT-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                            FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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CITY: Alexandria
STATE: Virginia
                                                                                                                  FILING DATE:
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              NAME: Teskin, Robin REGISTRATION NUMBER:
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LATHE, Richard
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O. Box 1404
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                          Robin L
NUMBER:
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FEATURE:

NAME/KEY: Peptide

COCATION: 1.21

OTHER INFORMATION:

OTHER INFORMATION:

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Best Local Similarity
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LOCATION: 144
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
NAME/KEY: Peptide
LOCATION: 147
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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LOCATION: 128.1727
OTHER INFORMATION: /r
OTHER INFORMATION: 12
OTHER INFORMATION: 2C
OTHER INFORMATION: refeature:
     361 PAPTTEKEPAPTTEK----KPAPTTEKEPAPTTEK----EPAPTTEKKPAPTAPKEPAPT 412
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                                                                                                                                                                                                                                                                                                                                                     134 P-KAETITKGP--ALTTPKEP-----TPTTPKEPASTTPKEPTPTTIKSAP 176
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LOCATION:
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OTHER INFORMATION:
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TYPE: amino acid
STRANDEDNESS: single
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                                                    APDXRP-XPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVT
                                                                                    TKEPSPTTPKEPAPTT--TKSAPTTTKEPAPTT----TKSAPTTPKEPSPTTTK----E
                                                                                                                      APDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS
                                                                                                                                                     PKE--PAPTTKEP-----APTTPKEPAPTAPK----KPAPTTPKEPAPTTPKEPAPTT 311
                                                                                                                                                                                                                                                      --DNKPAPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS
                                                                                                                                                                                                                     TKE--PAPTTT-----KSAPTTPKEPAPTTPK----KPAPTTPKEPAPTTPKEPTPTT
                                                                                                                                                                                                                                                                                             TTPKEPAPTTT-----KSAPTTPKEP----
                                                                                                                                                                                                                                                                                                                       PGSGSSTTQGQDVTLAPATEPASGSAATWGQDVTSVPVTRPALGSTTPPAHDVT---SAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.2%;
ilarity 24.4%;
Conservative (
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which is the codon for Pro or Ala wherein Pro =
or CCG; and Ala = GCT, GCC, GCA, or GCG."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Amino acids 1 to 21 are a 21 amino acid precursor sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Amino acid 144 is y = Xaa
which is the codon for Thr or Asn
or ACG; and Asn = AAT or AAC."
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which is the codon for
or CCG; and Ala = GCT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "The amino acids spanning 128 to 1727 constitute a repeated region wherein the repeat 20 amino acids, 17 of which are fixed. The number of such repeats varies from 1 to 40."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 423.5; DB 2; pred. No. 2.4e-19; 63; Mismatches 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            is X1 = Xaa
Pro or Ala wherein
GCC, GCA, or GCG."
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US-09-083-116-5
; Sequence 5, Application
; Patent No. 6203795
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                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
            CLASSIFICATION:
PRIOR APPLICATION DATA:
                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                 STATE: Virginia COUNTRY: United States ZIP: 22313-1404
                                                                                                                                                                                                                   STREET: P.O. Box
CITY: Alexandria
STATE: Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 618 KPAP--TTPK----ETAPTTPKEPAPTTP-----KKPAPTTPETPPPTTSEVSTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  572 KEPAPTTPKG----TAPTTLKEPAPTTP-----KKPAPKELAPTTTKGPTSTTSD 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              524
 APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPT-SRIAEAMLQTTTRPNQ 882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -TKPEMTTTAKDK----TTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTP-----KKPAPKELAPTTTKEPTSTTSDKPAP--TTPKGTAPTTPKEPAPTTP 571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAPDXRPXPGSTAPXAHGVTS----APDXRPXPGSTAPXAHGVTSAPDXRPX----PGST 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         926
                                                                                                                                                                                                                                                 P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                KIENY, Marie-Paule
LATHE, Richard
                                                                                             PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                    HAREUVENI, Mara
                                                                                                                                                                                                                                                                                                                                                                                                     CHAMBON,
                                                                                                                                                                                                                                                                 BURNS,
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                                                                                                                                                                                                                                                                                                 PHARMACEUTICAL COMPOSITION TREATMENT OR PREVENTION OF 5
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                                                                                                                                                                                                                                                                                                                                                                                                 Pierre
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                                                           US/09/083,116
08/479,537
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820 763 762 661

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LOCATION: 1..21
; OTHER INFORMATION: /
; OTHER INFORMATION: /
; OTHER STORMATION: 2.
US-09-083-116-5
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PRIOR APPLICATION UMBER: WO PCT/FR91/0083'
FILING DATE: 23-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,320
APPLICATION DATE: 04-APR-1993
                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1867 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
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OTHER INFORMATION:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
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                                                                                                                                        TSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKD-LAPTSKVLAKPT 133
                                                                                    P-KAETTTKGP--ALTTPKEP------TPTTPKEPASTTPKEPTPTTIKSAP 176
     --DNKPAPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS
                                TTPKEPAPTTT-----KSAPTTPKEP----
                                                        {\tt PGSGSSTTQGQDVTLAPATEPASGSAATWGQDVTSVPVTRPALGSTTPPAHDVT---SAP}
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linear
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147
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14-MAR-1995
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                                                                                                                 ---VTGSGHASSTPGGEKETSATQRSSVPSSTEKNAVSMTSSVLSSHS
                                                                                                                                                                                   8.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "The amino acids spanning 128 to 1727 constitute a repeated region wherein the repeat 20 amino acids, 17 of which are fixed. The number of such repeats varies from 1 to 40."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Amino acid 134
which is the codon for
or CCG; and Ala = GCT,
                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Amino acid 144 is Y = Xaa which is the codon for Thr or Asn wherein Thr or ACG; and Asn = AAT or AAC."
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                                                                                                                                                                                                                                                                                                                         /note= "Amino acid 147 is X2 = Xaa
which is the codon for Pro or Ala wherein Pro =
or CCG; and Ala = GCT, GCC, GCA, or GCG."
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21 amino acid
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                                                                                                                                                                        63;
                                                                                                                                                                        Score 423.5; DB 4;
Pred. No. 2.4e-19;
53; Mismatches 461;
                                                                                                                                                                                                                                                       acids 1 to
precursor s
                                  -----APTTTKEPAPTTPKEPAPTT 217
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Pro or Ala wherein Pro =
GCC, GCA, or GCG."
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                                                                                                                                                                Sequence 2, Application Patent No. 5861381
                                                                                                                                                    GENERAL INFORMATION:
                                                    APPLICANT: HAREUVENI
TITLE OF INVENTION: I
TITLE OF INVENTION: I
                                                                                                        APPLICANT:
APPLICANT:
             CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE,
STREET: P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361
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                                                                                                                                                                                                                                                                             884
Alexandria
                                                                  HAREUVENI, MATA
IVENTION: PHARMACEUTICAL COMPOSITION FOR THE
IVENTION: TREATMENT OR PREVENTION OF A MALIGNANT
                                                                                                          KIENY, Marie-Paule
LATHE, Richard
                                                                                                                                        CHAMBON,
                                                                                                                                       Pierre
                                                                                                                                                                                US/08479537A
                              SWECKER & MATHIS, L.L.P
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24
                                                           824 KPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPT-SRIAEAMLQTTTRPNQ 882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KPAP--TTPK----ETAPTTPKEPAPTTP-----KKPAPTTPETPPPTTSEVSTP 661
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                                                                                                                                                                                                                                                      DXRPXPGSTAPXAHGVTSAPDXRPXPGST--APXAHGVTSAPDXRPXPGSTAPXAHGVTS 820
                                                                                                                                                                                                                                                                                                                  -TKPEMTTTAKDK----TTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTS 763
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-GSTAPXAHGVTSAPDXRP--XPGSTAPXAHGVTSA-PDXRPXPGSTAPXAHGVTSAPDX 924
                                                                                                                                                                                   TTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQ 823
                                                                                                                              --STAPXAHGVT-----SAPDXRPXPGSTAPXAHGVTSAPDXRPXP- 868
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STATE: Virginia

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NAME/KEY: Peptide
LOCATION: 1..21
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
   Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2035 amino acids
                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: ...
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 90/13101
FILING DATE: 23-CCT-1990
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 04-APR-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                     NAME/KEY: Peptide LOCATION: 144
OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                        OTHER INFORMATION:
                                                                                                                                                                                       OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                         LOCATION:
                                                                                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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134
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128..1899
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14-MAR-1995 .
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     8.2%;
                                                                                                                                                                  /note= "Amino acid 147 is X2 = Xaa which is the codon for Pro or Ala wherein Pro = or CCG; and Ala = GCT, GCC, GCA, or GCG."
                                                                                                                                                                                                                                                                      /note= "Amino acid 144 is Y = Xaa
which is the codon for Thr or Asn
or ACG; and Asn = AAT or AAC."
                                                                                                                                                                                                                                                                                                                                                                     /note= "Amino acid 134 is X1 = Xaa Xaa Xaa Which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA, or CCG; and Ala = GCT, GCC, GCA, or GCG."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note- "The amino acids spanning 128 to 1899 constitute a repeated region wherein the repeat 20 amino acids, 17 of which are fixed. The number of such repeats varies from 1 to 40."
                                                                                     /note= "Amino
21 amino acid
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                                TP 884
                                                                                                                                                                                                                            -TKPEMTTTAKOK----TTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTS
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                                                                -GSTAPXAHGVTSAPDXRP--XPGSTAPXAHGVTSA-PDXRPXPGSTAPXAHGVTSAPDX
                                                                                          KPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPT-SRIAEAMLQTTTRPNQ 882
                                                                                                                                APDXRPXPG
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                                                                                                                                                                                             DXRPXPGSTAPXAHGVTSAPDXRPXPGST--APXAHGVTSAPDXRPXPGSTAPXAHGVTS
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Sequence 2, Application US/09083116 Patent No. 6203795
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APPLICANT: CHAMBO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 0: FILING DATE: 14-MAR-1995 ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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              FEATURE
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LOCATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Alexandria
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VENTION: PHARMACEUTICAL COMPOSITION FOR THE
VENTION: TREATMENT OR PREVENTION OF A MALIGNANT
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14-MAR-1995
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2:
                               /note= "Amino acid 144 is Y = which is the codon for Thr or or ACG; and Asn = AAT or AAC."
                                                                                                                                                                                                                       /note= "The amino acids spanning 128 to 1899 constitute a repeated region wherein the repeat 20 amino acids, 17 of which are fixed. The number of such repeats varies from 1 to 40."
                                                                                                                          /note= "Amino acid 134 is X1 = Xaa
Xaa Xaa which is the codon for Pro or
CCC, CCA, or CCG; and Ala = GCT, GCC,
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Best Local Similarity
Matches 235; Conserv
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                               DXRPXPGSTAPXAHGVTSAPDXRPXPGST--APXAHGVTSAPDXRPXPGSTAPXAHGVTS
                                                          -TKPEMTTTAKDK----TTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTS
                                                                                          {\tt DXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAP}
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TTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQ
                                                                                                                        TTTKEPTT-----IHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAA---
                                                                                                                                                     RPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGS--TAPXAHGVTSAP
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21 amino acid
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which is the codon for
or CCG; and Ala = GCT,
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Pred. No. 2.6e-19;
3; Mismatches 461;
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GCC, GCA, or GCG."
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US-08-276-967-2
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                                                                                                                                                                                                                                                                             Query Match
8.1%; Score 419.5; DB 2; Length 2476;
Best Local Similarity 32.5%; Pred. No. 5.7e-19;
Matches 163; Conservative 43; Mismatches 177; Indels 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08276967 Patent No. 5851817
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 2476 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Hardy, Daniel M.
APPLICANT: Garbers, David L.
TITLE OF INVENTION: Species-Specific Egg-Binding Proteins of
TITLE OF INVENTION: Sperm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 713-789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UTSD
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,967
FILING DATE: Submitted Herewith
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
581 GTAPTTLKEPAPTTPKKPAPKELAPT-TTKGPTSTT---SDKPAPTTPKETAPTTPKEPA 636
                                                                                                                                             466 APTTPKAAAPNIPKEPA----PITPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEP 521
                                                                                                                                                                                                            313
                                                                             522 APTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAPT-TPKEPAPTTPKEPAPTTPK 580
                                                                                                                  366 TIPTEKSTVPT--KKPTVFKEPTLPPE-GPTVPAE-RPTTPPEGPAVPPKG--PTVLTE- 418
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77D: 77210-4433
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STATE: Texas
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                                       ------WPTSHTEKSTVHTEKPILPTGKSTIPTEKPMVPTKRT-----TTP- 458
                                                                                                                                                                                               PSETSVSTEKPVAPTE----KPTVPSEIYTIPTEKPMVHMEKPIVHT--EKPTVPT-EKP 365
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                                                                                                                                                                                                                                                                              637 PTTPKKPAPTTPETPPP-----TTSEVSTPT-----TYKEPTTIHKSPDESTPELSAEPT 686
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                                                                               KPKDRATNSKATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPT 866
                                                            AP-----TTPQP-SPTLVPTQPAAVVMPST-----SATTVTPRTTIASCP---PN 693
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Search completed: April 26, 2002, 16:17:05 Job time: 216 sec

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OM protein -
protein search, using sw model
                                            Copyright
                                          GenCore version
(c) 1993 - 2000
                                                       4.5
                                         Compugen Ltd
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April 26, 2002, 16:19:22 ; Search time 82.85 Seconds 931.380

(without

alignments)

Million cell updates/sec

Title: Perfect score: Sequence: US-09-556-246-1_COPY_200_1212 5416 VKDNKKNRTKKKPTPKPPVV...... SPIDTVFTRCNCEGKTFFFK 1013

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Maximum 80 80 seq seq length: 0 length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s

summaries

PIR_68:* pir1:*
pir2:*
pir3:*
pir4:*

Database

Pred. No. score grea and is der No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution.

SUMMARIES

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A43427	A54641	T31113	A45155	T45463	A37221	T45462	S70795	T32271	JQ0985	A47282	JH0557	T27642	QFMSH	JU0465	S20500
neurofilament trip	interspersed repea	mucin-like glycopr	mucin FIM-C.1 - Af	membrane glycoprot	neurofilament trip	membrane glycoprot	vsaA protein precu	hypothetical prote	hydroxyproline-ric	calcium-binding pr	exo-alpha-sialidas	hypothetical prote	neurofilament trip	extensin precursor	hydroxyproline-ric

ALIGNMENTS

mucin 2 precursor, N;Alternate names: intestinal - human (fragments)

N;Alternate names: mucin SMUC-41
(;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 10-Mar-1993 #sequence_revision 12-Apr-1996 #text_change 05-Nov-1999
C;Accession: A49963; A45106; B45106; A43932; B33532; A61257; PQ0328; PQ0329
C;Accession: A49963; A45106; B45106; A43932; B33532; A61257; PQ0328; PQ0329
C;Accession: A49963; A45106; B45106; A43932; B33532; A61257; PQ0328; PQ0329
C;Accession: A49963; A45106; A4701bara, N.W.; S1ddiki, B.; Kim, Y.S.
J. Biol. Chem. 269, 2440-2446; 1994
A;Title: Molecular cloning of human intestinal mucin (MUC2) cDNA. Identification of t

A; Reference number: A49963; MUID: 94132002 A; Accession: A49963

A; Molecule type: mRNA A; Residues: 1-639 <GU1>

A;Cross-references: GB:L21998

R;Gum Jr., J.R.; Hicks, J.W.; Toribara, N.W.; Rothe, E.M.; Lagace, J. Biol. Chem. 267, 21375-21383, 1992
A;Title: The human MUC2 intestinal mucin has cysteine-rich subdoma. R.E.; Kim, Y.S.

A;Reference number: A45106; MUID:93016075 A;Accession: A45106 mucin has cysteine-rich subdomains located both up

A;Status: not compared with conceptual translation

A; Molecule type: mRNA A; Residues: 626-1895 < GU2>

A;Cross-references: GB:M94131; NID:g186395; PIDN:AAA59163.1; PID:g186396 A;Note: sequence extracted from NCBI backbone (NCBIP:116706)

A; Accession: B45106

A; Molecule type: mRNA A; Residues: 2037-3020 <GU3>

A:Status: not compared with conceptual translation

A; Experimental source: colon A;Cross-references: GB:M94132; NID:g186397; PIDN:AAA59164.1; PID:g186398

A;Note: sequence extracted from NCBI backbone (NCBIP:116698)
R;Toribara, N.W.; Gum Jr., J.R.; Culhane, P.J.; Lagace, R.E.; Hicks, J.W.; Petersen, J. Clin. Invest. 88, 1005-1013, 191.
J. Clin. Invest. 88, 1005-1013, 191.
A;Title: MUC-2 human small intestinal mucin gene structure. Repeated arrays and polym A;Reference number: A43932; MUID:91358717
A;Accession: A43932

A:Molecule type: DNA
A:Molecule type: DNA
A:Residues: 1343-1350, 'L', 1352-1411,'S', 1413-1448,'P',1450-1503,'T',1505-1915 <TOR>
A:Residues: 1343-1350, 'L', 1352-1411,'S', 1413-1448,'P',1450-1503,'T',1505-1915 <TOR>
A:Roos: references: GB:M74027; NID:g188863; PIDN:AAA58875.1; PID:g188864
A:Note: sequence inconsistent with the nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:55749, NCBIP:55750)
R:Gum, J.R.; Byrd, J.C.; Hicks, J.W.; Toribara, N.W.; Lamport, D.T.A.; Kim, Y.S.
J. Biol. Chem. 264, 6480-6487, 1989
A:Title: Molecular cloning of human intestinal mucin cDNAs. Sequence analysis and e. A:Reference number: A33532; MUID:89197956
A:Accession: B33532 Sequence analysis and evi

A;Molecule type: mrNA A;Residues: 1916-2193 <GU4> A;Cross-references: GB:M22405; NID:g188873; PIDN:AAA36334.1; A; Experimental source: intestine PID:g188874

Gallup, M.W.; Yan, P.S.; Gum, J.R.; Kim, Y.S.; Basbaum, C.B.

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J. Clin. Invest. 87, 77-82, 1991
A;Title: Human bronchus and intestine express the same mucin gene.
A;Reference number: A61257; MUID:91086481
A;Accession: A61257
A;Status: not compared with conceptual translation
A;Molecule type: mRMA
A;Residues: 'T',1925-1948,'TTS',1952-1954 <JAN>
A;Experimental source: bronchus
R;Xu, G.; Human, L.; Khatri, I.; Sajjan, U.S.; McCool, D.; Wang, D.; Jones, C.; Forstner, R;Xu, G.; Human intestinal mucin-like protein (MLP) is homologous with rat MLP in the C-t A;Reference number: PQ0328; MUID:92188477
A;Residues: 2328-2468 <XUG>
A;Molecule type: mRMA
A;Residues: 2328-2468 <XUG>
A;Accession: PQ0328
A;Cross-references: GB:M6523
A;Cross-references: small intestine
A;Residues: 2328-2342,'K',2344-2354 <XUGI>
A;Genetics:
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A;Genetics: GDB:MUC2
A;Cross-references: GDB:120203; OMIM:158370
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   PLPPSITPPTFSPFSTTTPTTPCVPLCNWTGWLDSGKPNFHKPGGDTELIGDVCGPGWAA 1819
                                                                     PKEPAPTTP----KETAPTTP-----
                                                                                                                                               PTTTPSSPITTTTPSSTTTP-SPPPTTMTTPSPTTTPSPPTTTMTTLPPTTTSSPLTTT 1759
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C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C;Accession: T31108
R;Goernhardt, B.
submitted to the EMBL Data Library, April 1998
A;Reference number: Z20986
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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vative 46; Mismatches 475;
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hypothetical protein F35A5.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Cpate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #tc;Accession: T16251 R;Leimbach, D. R;Leimbach, D. Submitted to the EMBL Data Library, January 1996 A;Description: The sequence of C. elegans cosmid F35A
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A;Residues: 1-1274 <LEI>
A;Cross-references: EMBL:U46675; NID:gl166613; PID:gl166621; PIDN:AAB52641.1; GSPDB:GN0(A;Experimental source: strain Bristol N2; clone F35A5
C;Genetics:
A;Gene: CESP:F35A5.1
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                                                                                                                                                                                                                                                                                                                                                                                                APTAPKKPAP-----TTPKEPAPTTPKEPAPTTTKEP----SPTTPKEPAPTTTKSAPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PKKAAPAVKPRDSSPKKATPLQADPKAQEVPPTPVKNPVKKYKPPWEVDDEDPVEEVKQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ETQSIEKTSAKDLAPTSKVLAKPTPKAE----TTTKGPA--
                                                                                                                                                                                                                     T--EVPPAVVKKPEPVAKSRDPSPKKAK-AEPNSP--VVPPTPVKNPVKKWKPPWEDDDA
                                                                                                                                                                                                                                                                                         PEKK-TPVLAKKAPTKPDSEAAADPVSGPSSKDPKLAKKAPVKPRDPSPMKAVPIKPAPK
                                                                                                                                                                                                                                                                                                                             TTKEPAPTTTKSAPTTP-KEPSPTTTKEPAPTTPK--EPAPTTPKKPAP--TTPKEPAPT
                                                                                                                                                                                                                                                                                                                                                              KEPTPTTP----KEPASTTPKEP----TP-TTIKSAPTTPKEPAPTTTKSAPTTPKEPAP
   K-KEPEKPKD-APKVAAKPRDPSPKKAVPE--KEPAKVAAKPRDLSPKKAIPIPANTQEA
                                   KGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPT----TPKKPAP----
                                                                       PSPKKAEPNSPVVP----PTPVKNPVKKW-KPPWEDDDEPTEEVKKPSE--PEKKTPVLA
                                                                                                         PAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPT-TTKEPTSTTSDKPAPTTP
                                                                                                                                               PAEPVNVPEPEKKTPVLAKKTPVKPRDPSPKKAVPAKPSTKTDAPPVSVKKPEPVSKPKE
                                                                                                                                                                                 PTTPEELAPTTPEEP-----TPTTPEEPAPTTPKAAAPNTPKEPAPTTPKEPAPTT-PKE
                                                                                                                                                                                                                                                       TPKEPAPTTTKKPAPTA-PKEPAPTTPKETAPTTPKKLTPTTP----EKLAPTTPEKPA
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90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.8%; Score 802; DB 2; 28.0%; Pred. No. 1e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -PTTPKEPAPTTTKEPAPT----TTKSAPTTP
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A;Cross references: EMBL:x13857; NID:g4551; PIDN:CAA32069.1; R;Lambrechts, M.G.; Bauer, F.F.; Marmur, J.; Pretorius, I.S. Proc. Natl. Acad. Sci. U.S.A. 93, 8419-8424, 1996
A;Title: Mucl, a mucin-like protein that is regulated by Mssl A;Reference number: JC6123; MUID:96323237
A;Accession: JC6123

Mss10,

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critical for

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A; Molecule type: DNA A; Residues: 1-31 <PAR>

A; Accession: S27281

A;Gene: SGD:MUC1; STAZ; MAL5; DEXZ; SGD:SUUU14 A;Cross-references: MIPS:YIR019c; SGD:S0001458 A;Map position: 9R

SGD:MUC1; STA2; MAL5; DEX2; SGD:S0001458

GB:U30626; NID:g1304386; PIDN:AAC49609.1;

PID:g1304387

A; Molecule type: DNA A; Residues: 1-1367 <

A; Status: nucleic acid sequence not shown

A;Cross-references:

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RESULT 5
$48478
$48478
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$48478
$10can 1,4-alpha-glucosidase (EC 3.2.1.3) - yeast (Saccharomyces cerevisiae)
N;Alternate names: extracellular glucoamylase; mucin-like protein MUC1; prot
C;Speciles: Saccharomyces cerevisiae
C;Speciles: Saccharomyces cerevisiae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 12-Nov-1999
C;Accession: $48478; A26877; B26877; $27281; JC6123
R;Rowley, K.
R;Rowley, K.
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J. Bacteriol. 169, 2142-2149, 1987
A;Title: Gene fusion is a possible mechanism
A;Reference number: A91831; MUID:87194600
A;Accession: A26877
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A;Cross-references: EMBL:M16165; NID:g172523; PIDN:AAA35015.1; R;Pardo, J.M.; Innez, E.; Zalacain, M.; Claros, M.G.; Jimenez, FEBS Lett. 239, 179-184, 1988 and the 5' regions of the STA2 a;Title: Similar short elements in the 5' regions of the STA2 a;Reference number: S27281; MUID:89031230
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                                                                                                              A; Molecule type: DNA
A; Residues: 762-1331 <YA2>
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A; Residues; 1-1367 < ROW>
A; Cross-references: GB:Z47047; EMBL:Z38061;
A; Cross-references: nakamura, M.; Fukui, S.
                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type:
A; Residues: 1-13
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C:Superfamily: yeast glucan 1,4-alpha-glucosidase homolog; glucan 1,4-alpha-glucosidase C:Keywords: glycosidase; hydrolase; polysaccharide degradation; transmembrane protein F;5-21/Domain: transmembrane #status predicted <TM1>
F;1350-1366/Domain: transmembrane #status predicted <TM2>
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   -SVTTVTNFTPTT-ITTTVCSTGT--
                                                                                                                VPTTTTTSVTTSSTTTITTTVCSTGTNSAGETTSGCSPKTITTTVPCSTSPSETA----
                                                                                                                                   --TTQVTSTTTQOTTPFKITTLKTTTLAPKVTT---TKKTITTT-EIMNKPEETAKPKDR
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                           KMTSTMPELNPTSRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -TTPKEPAPT-TPKKPAPTTPKEPAPTTPKEPAPTTTKKPAPTAPKEPAPTTPKETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative 104; Mismatches 483; Indels 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.6%; Score 789.5; DB 1; 28.4%; Pred. No. 3.8e-27;
                                                                                    ----TKAPKKPTSTKKPKTMPRVRKPKTTPTPR
NSAGETTSGCSPKTVTTTVPCST 1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1367;
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                                                         1077
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extensin-like protein - maize
C;Species: Zea mays (maize)
C;Date: 05-Mar-1995 #sequence_revision 12-May-1995 #text_change
C;Accession: $49915
R;Rubinstein, A.L.; Broadwater, A.H.; Lowrey, K.; Bedinger, P./
submitted to the EMBL Data Library, June 1994
A;Description: Pex genes: pollen-specific genes with extensin-la;Reference number: $49915
A;Reference number: $49915
A;Accession: $49915
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1188 <RUB>
Ş
                                                                                                                                                                                                                                                                                                                                                                                              RESULT
S49915
                                                                                                                                A;Cross-references: EMBL:Z34465; NID:g600117; PIDN:CAA84230.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B
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                      Query Match
Best Local Similarity 29.9
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FMPEVTPDMDYLPRVPNQGIIINPMLSDETNICNGKPVDGLTTLRNGTLVAFRGHYFWML
                                                                                                                                                                                                                                                                                                                           #sequence_revision 12-May-1995 #text_change
                          14.5%; Suc.
29.9%; Pre-
                                  Score 784; DB 2; 1
Pred. No. 5.7e-27;
9; Mismatches 359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1009
                                                                       Length 1188;
                                                                                                                                                                                                                                                   extensin-like
                                    Indels 122;
                                                                                                                                PID:9600118
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                                Gaps
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                                  33;
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В В δÃ δÃ В Вb ρy В Q QΥ 밁 Ъ Š 밁 564 944 518 988 459 828 412 769 352 719 292 660 600 241 184 542 129 460 13 69 -KEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPT LAPKSSPPHVVVSSPPPVVKSSPPPAPVSSPPLTPKPASPPAHVSSPPEVVKPSTP--PA EPSPTTTKEPAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTTTKKPAPTAPKEPAP VKSSPPPAPVSSPPATPKSSPPPAPVNLPPPEVKSSPPPTPVSSPPPA---PKSSPPPAP LKE---PA-----PTTPKK----PAPKELAPTTTKE----PTSTTSDKPAPTTPKGTAPTTP PTTVISP-PSEPKSSPPPTPVSLPPPIVKSSPPPPAMVSSP-PMTPKSSPPPVVVSSPPPT TTPKETAP----TTP----KKLTPTTPEKLAPTTPEKPAP----TTPEELAPTTPEEPT PPAPLSSPPPAPQVKSSPPPVQVSSP-PPAPKSSPPLAPVSSPPQVEKTSPPPAPLSSPP PTTPEEPAPTTPKAAAPNTPKE-PAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTT SP--PKEPVSSPPQTP----KSSPPPAPVSSPPPTPVSSPPALAPVSSPPSVKSSP----PAKSTPPPEEYPTPPTSVKSSPPPEKSLPPPTLIPSPPPQEKPTPPSTPSKP-PSSPEKP PKKPAPTTPKEPAPTT-----PKE---PTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKP PTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRPSL----PPN 68 **APTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPK** PPAPVASPPPPVKSPPPPTPVASPPPPAPVASSPPPMKSPPPPTPVSSPPPPEKSPPPPP PTTTKSAPTTP--KEPAPTTTKEPAPTTPKEPAPTTTKEPAPTTTKSAPTTP-KEPAPTT SPPPPVKSPPPPAPVGSPPPPEKSPPPPAPVASPPPPVKSP--PPPTLVASPPPPVKSPP 599 ----LAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAPTTPKEPA 183 SDTSKETSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKV 128 PTPHSPPAD------DYVPPTPPVPGKSPPATSPSPQVQPPAASTPPPSLVKLSPPQ 510 -SPPPPVKTTSPPAPIG----SPSPPPPVSVV 411 351 458 768 291 541

Ş В δõ Ъ ρy Qy

Qy 397	Qy 358 Db 1210	Qy 312 Db 1150	Qy 258 Db 1090	Oy 222 Db 1033	Qy 172 Db 973	Qy 145 Db 914	Qy 85 Db 858	Qy 34 Db 806	Query M Best Lo Matches	C;Genetics: A;Gene: Naca A;Gene: Naca A;Map positi A;Introns: 2 A;Introns: 2 A;Note: diff C;Keywords:	A; Status: A; Molecul A; Residue	R; Yotov, W. Genes Dev. A; Title: Di A; Reference	Species Date:	RESULT T30826 nascent F	Qy 682 Db 1116	Qy 623 Db 1058	
97 TTKKPAPTAPKEPAPTTPKETAPTTPEKKLTPTTPEKLAPTTPEK-PAPTTPEELAPTTPE 455	58 TKEPADTTPKEPAPTTPKKPAPTTPKE	12 TKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTT-KSAPTTPKEPSPTT 357	58 KEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAPTTPKEPAPTT 311	22 APTTTKSAPTTPKEPAPTTPKK-PAPTTPKEPAPTTP 257	72 IKSAPTTPKE-PAPTTTKSAPTTPKEPAPTTTKEPAPTTPKEPAPTTTKEP 221 : :	5 LTTPKEPTPTTPKEPASTTPKEPTPTT 171	35 VETKETTITNKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPÅ 144 	34 VTTPDTSTTQHNKVSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETT 84	CD	on: 10 4/1; 1996/1; 2024/3; 2050/3; 2099/3; 2142/3; 2183/3 erential splicing converts alphaNAC into a tissue-specific alternative splicing; DNA binding; transcription factor	Status: preliminary; translated from GB/EMBL/DDBJ Molecule:type: DNA Molecule:type: DNA Residues: 1-2187 < YOT> Cross-references: RMRL:U48363: NID:q1666688; PID:q1666689; PIDN:AAB18732.1	YOTOV, W.; St-Arnaud, R. YOTOV, W.; St-Arnaud, R. nes Dev. 10, 1763-1772, 1996 Title: Differential splicing-in of a proline-rich exon converts alphaNAC into a muscle Reference number: 220889; MUID:96312450	();Alternate names: alpha-NAC process C;Species: Mus musculus (house mouse) C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 24-Nov-1999 C:Accession: T30826	associate	2 SAEPTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPET 731	3 -TPKETAPTTPKEPAPTTPKKPAPTTPETPPPTISEVSTPTITKEPTIIKSPDESTPEL 681 	

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                                                                                                        APKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPNQTPNSK 887
                                                                                                                                                                              DTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQKPTK 827
                                                                                                                                                                                                                    T--SLAQTAPPSLQKAPSTTIPKENLAAPAV----LPVSSKSPAAPARASASLSPATAAP 1665
                                                                                                                                                                                                                                                                                            KNPSSHKKTSKTIELKEAPATLPPSPTKSPKIPSSKKAPRT--SAPKEFPASPSIK-PVT 1611
DSHISPVS-DACSTGTTTP 1770
                                  LVEVNPKSEDAGGAEGETP
                                                                                                                                                                                                                                                       TKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTSTTTQ 767
                                                                                                                                                                                                                                                                                                                               TSEVSTPTTTK-----EPTTIHKSPDESTPELSAEPTPKALENSPKE-PGVPTTKTPAA 707
                                                                                                                                                                                                                                                                                                                                                                    PKTAAPPSER-VTTVPPEKPA-TPQKASGTTASKVPVPAETQEVAVSSRETPVTPAVPPV 1554
                                                                                                                                                                                                                                                                                                                                                                                                 PKELAPTITKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPTTPETP-----PPT 654
                                                                                                                                                                                                                                                                                                                                                                                                                                         VGPKETSLEGATAVPLEIPPSHKKAPKTVDPKQVPLTPSPK-DAPTTLAE-SPSSPKK-A 1496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---TTSDKPAPTTPKGTAPTTPKEPAPTTPKE-PAPTTPKGTAPTTLKEPAPTTPKKPA 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPTPTT-----PEEPAPTTPKAAAPNTPKEPAPTTPKE-PAPTTPKEPAPTTPKETA 506
                                                                           -PKKASSSKRASTLP
                                                                                                                                                 QTAPKEATTIPSCKKAAATETPIETSTAPSLEGAPKETSE----TSVSKVLMSSP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSPRKGSKKAGSKE-TPTTPSPEGVTAAPLEIPISSKKTSKMASPKETLVTPSSKKLSQT 1439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTTPKGTAPTTLKEPAPTTP----
                                      906
                                                                             ATTLPSLKEASVLS --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -KKPAPKELAPTTTKEPTS--
                                                                           -PTATSSGK 1752
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                                                                                                                                                      1716
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mucin 1 precursor, repetitive splice form A [validated] - human N;Alternate names: breast carcinoma-associated DF3 antigen; core protein KF39; episla ncreatic mucin; polymorphic epithelial mucin (PEM) N;Contains: mucin 1 precursor, epithelial tumor antigen splice form; mucin 1 precurso C;Species: Homo sapiens (man) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Jun-2000 C;Date: 20-Apr-3000 #sequence_revision 20-Apr-2000 #text_change 02-Jun-2000 C;Accession: A35175; B35175; B35886; A35887; S10572; S40293; A36735; PX00666; S10218; R;Liqtenberg, M.J.L.; Vos, H.L.; Gennissen, A.M.C.; Hilkens, J. J. Biol. Chem. 265, 5573-5578, 1990 A;Title: Episialin, a carcinoma-associated mucin, is generated by a polymorphic gene A;Accession: A35175; MUID: 90202794 A; Molecule type: mRNA, A; Molecule type: mRNA, A; Residues: 1-952,1033-1344 <LIG1> A; Residues: 1-952,1033-1344 <LIG1> A; Residues: 1-952,1033-1344 <LIG1> A; Cross-references: GB:M32738; GB:J05288; NID:g182121; PIDN:AAA35804.1; PID:g182124; A; A; Cross-references: GB:M32738; GB:J05288; NID:g18212121; PIDN:AAA35804.1; PID:g182124; A; A; Cross-references: GB:M32738; GB:J05288; NID:g182121; PIDN:AAA35804.1; PID:g182124; A; A; Cross-references: GB:M32748; A; Cross-references: A; Accession: B35175 amino-and carboxyl

A;Molecule type: mRNA
A;Residues: 1-19,29-95;1033-1344 <LIG2>
A;Cross-references: GB:M32739; GB:J05288; NID:g182126; PIDN:AAA35806.1; PID:g182129;
A;Cross-references: GB:M32739; GB:J05288; NID:g182126; PIDN:AAA35806.1; PID:g182129;
A;Experimental source: splice form B
A A; Molecule type: mRNA A; Residues: 1-19, 29-992, 1033-1344 A; Cross-references: GB:J05581; NII NID:g188869; PIDN:AAA59876.1; PID:g188870 <GEN> of human tumor-associated polymorphic epith

27.8%;

Pred.

Mismatches No.

56;

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A:Note: undetermined tyrosine residues in the carboxyl-terminal non-repetitive C:Comment: This protein is length polymorphic. Individuals may have between 21 partial repeats. The repeat shown is defined by SmaI nuclease sites. C:Comment: Serine and threonine residues in the tandem repeat domain are extens C:Comment: For an alternative splice form without a tandem repeat domain, see I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-142, 'Q', 144-162, 'Q', 164-168 < ABES:
A; Cross-references: EMBL: M31823; NID: g181542; PIDN: AAA35757.1;
A; Cross-references: EMBL: M31823; NID: g181542; PIDN: AAA35757.1;
A; Masuzawa, Y; M1yauchi, T; Hamanoue, M.; Ando, S.; Yoshida,
J. Blochem. 112, 609-615, 1992
A; Title: A novel core protein as well as polymorphic epithelial
A; Reference number: JX0235; MUID: 93123189
A; Accession: PX0066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Molecule type: mRNA
A:Residues: 1-19,29-155,'p',157-175,'p',177-182,'A',184-212,1033-1037,'A',1039-1344 <WR:
A:Residues: 1-19,29-155,'p',157-175,'p',177-182,'A',184-212,1033-1037,'A',1039-1344 <WR:
A:Cross-references: EMBL:x52229; NID:g37053; PIDN:CAA36478.1; PID:g37054
R:Abe, M.: Siddiqui, J.; Kufe, D.
Biochem. Biophys. Res. Commun. 165, 644-649, 1989
A:Title: Sequence analysis of the 5' region of the human DF3 breast carcinoma-associated A:Reference number: A36735; MUID:90088473
A:Accession: A36735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-19,29-1109,'S',1111-1339,'A',1341-1344 <LAN>
A; Residues: 1-19,29-1109,'S',1111-1339,'A',1341-1344 <LAN>
A; Cross-references: GB:J05582; NID:g189598; PIDN:AAA60019.1;
A; Note: GenBank entry HUMPANNU contains four fewer copies of
A; Note: GenBank entry HUMPANNU contains four fewer copies of
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: Tyrosine phosphorylation of the MUC1 breast A; Reference number: S51026; MUID: 95080414 A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 998-1011, 'ES', 1014-1017;1018-1032, 'T', 1034-1037;1038-1057
A; Experimental source: gastric carcinoma cell
R; Zrihan-Licht, S.; Baruch, A.; Elroy-Stein, O.; Keydar, I.; Wreschner
FEBS Lett. 356, 130-136, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-19, 29-155, 'P', 157-175, 'P', 177-182, 'A', 184-212, 1033-1344
A: Cross-references: EMBL: X52229; NID: 937053
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Eur. J. Biochem. 189, 463-473, 1990
A:Title: Human epithelial tumor antigen cDNA sec
A:Reference number: S10571; MUID:90276413
A:Accession: S10572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Note: GenBank entry HUMMUCAB includes one copy of the tandemly repeated sequence R:Lan, M.S.; Batra, S.K.; Q1, W.N.; Metzgar, R.S.; Hollingsworth, M.A.
J. Biol. Chem. 265, 15294-15299, 1990
A;Title: Cloning and sequencing of a human pancreatic tumor mucin cDNA.
A;Reference number: A35887; MUID:90368716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: A35887; MUID:90368716
A;Accession: A35887
A;Status: not compared with conceptual translation
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     12.4%;
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   Score
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   672;
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   DВ
 1;
Length 1344;
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J.; Takao,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mucin carry peanut
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proteins
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                                                                                                                                                                                           TLKTTTLAPKVTTTKKTITTT--EIMNKPEETAKPKDRATNSKATTPKPQKPTKAPKKPT
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                                                                                                                                                                                                                                                                                         -TAAPKMTKETATTTEKTTESKITATTTQVTSTTTQDTTP--FKIT
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RESULT 9
T18535
T18535
Allow molecular mass nuclear antigen - chicken C;Species: Gallus gallus (chicken)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-
C;Accession: T18535
- 20 T18535
- 20 T18535
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A;Molecule type: mRNA
A;Residues: 1-1151 <SHI>
A;Cross-references: EMBL:D88440; NID:d1177138; PID:d1025045; PIDN:BAA24137.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: Z18955; A; Accession: T18535
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                                                                                                                                                                                                                                                                                                                                                                               EPAPTTPKEPAPTTTKEPAPTTTKSAPTT-----PKEPA-----PTTPKKPAPTTPK
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                                                                                                                                                                                        PGVPNAATDPQKPPPTPQSVPSAVTEPKPQPRAAPPPSNEATPAVPSPSPNLKSPLPTIP
                                                                                                                                                                                                                   P----APTTPKEPAPTTPKKPAPTTPKEPAP-----TTPKEPAPT-TTKKPAPTAP 406
                                                                                                                                                                                                                                             PVTKAATTTNATPPPQPIPKAATTTTATPVTPQQPIPKAGTDAAPPPAVPKAPSDGRAAT
                                                                                                                                                                                                                                                                       P---APTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAP---TTTKSAPTTPKEPSPTTTKE
                                                                                                                                                                                                                                                                                                 -TAGAVPKASTGTTPAAAPQQPVP---KAAPVTPPSPQQAVPRAATAAA----APVTPQQ
                            TLMAPMGAANTQMAPIGAAGAAQTAPMGAAHTHVSPMGAGGATQMSPTGAANTHMSPIGA
                                                                                LPSSPVASAMHAKVTPRPLPASPVPMAASPASLGPDAARVALATNAASPGAKPEAAGGNG
                                                                                                                                                              K-----EPAPTTPK---ETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELA-----
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                                                                                                                                      KPVPLMALTPQPVTAQMVTQLAATKPSPIVPKASPK-ALMTPPPPPPGLPRALAAAKLLG
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                                                     PAPTTPKEPAPTTPKEPAPTTPKETAPT----
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 TLKEPAPTTPKKPAPKELAPTTTKEP--
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                                                                                                                                                                                                                                                                                                                                                                                                                                    -TKSAPTTPKEPAPTTTK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           %; Score 671; DB 2; Length 11
%; Pred. No. 3.9e-22;
100; Mismatches 419; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1151;
                                                                                                             -KAAAPNTPKE----
                                                          -TPKGTAPT-----
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    -TSTTSDKPAPTTP
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hypothetical protein F16F9.2 - Caenorhabditis elegans C.Species: Caenorhabditis elegans C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te C.Accession: T25697 R.Fulton, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:U67956; PIDN:AAB07691.1; GSPDB:GN00028; CESP:F16F9.
A;Experimental source: strain Bristol N2; clone F16F9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated
A;Molecule type: DNA
A;Residues: 1-1229 <FUL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, August A; Description: The sequence of C. elegans of the control of the con
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A; Introns: 35/1; 361/1; 384/1; 482/2; 517/1;
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                                                                                                                                                                                                      KETTVETKETTTINKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTT 140
                                                           KGPALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAPTTPKEPAPTTTKSAPTTPKEPAPT
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Pred. No. 1.3e-21;
8; Mismatches 339;
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TTEEPTPTTTEE--VTTTEAETSTTTSSETSTEK---PTTPLIDNKIAGPATGK---PET TTKEPAPTTPKEPAPTTTKEPAPTTTKSAPTTPKEPAPTTP----KKPAPTTPKEPAPTT 256

324

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extensin class 1 precursor - cowpea
C.Species: Vigna unguiculata (cowpea)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 17-1
C;Accession: T11622; S54155
R;Arsenijevic-Maksimovic, I.; Broughton, W.J.; Krause, A.
Mol. Plant Microbe Interact, 10, 95-101, 1997
A;Title: Rhizobia modulate root-hair-specific expression of extensil A;Reference number: Z17301; MUID:9715574
A;Accession: T11622
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-489 <ARS>
A;Cross-references: EMBL:X91836; NID:g1015936; PIDN:CAA62943.1; PID
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                                                                                                                                                                                                                                                                                                                                               -----INNTQISQPKPTDISKTDALSSLISGLIGSFTKAPMAPTI-
                                                                                                                                                                                                                                                                                                                                                                               TAKPKDRATNSKATTPKPQ----
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A;Experimental source: sub_species Red caloona
R;Arsenijevic-Maksimovic, I.; Broughton, W.J.; Krause, A.
submitted to the EMBL Data Library, April 1995
A;Description: A class of root-hair specific extensins inv
A;Reference number: S54155
A;Accession: S54155
A;Accession: S54155
A;Accession: S54155
A;Refinanary
A;Molecule type: mRNA
A;Residues: 326-489 <AR2>
A;Cross-references: EMBL:X86030; NID:g791149; PID:g791150
C;Genetics:
A;Gene: Exr26G
C;Superfamily: hydroxyproline-rich glycoprotein
C;Keywords: glycoprotein; hydroxyproline
E;1-2yDomain: Signal sequence #status predicted <NAT;
F;24-489/Product: extensin class 1 #status predicted <MAT;
A; Molecule type: mRNA
A; Residues: 1-7962 <R:
A; Cross-references: El
C; Genetics:
                                                                                        R:Labeit, S.; Kolmerer, B.
Science 270, 293-296, 1995
A;Title: Titins: giant proteins in charge
A;Reference number: A57430; MUID:96026330
A;Accession: I38346
                                                                                                                                                                                      elastic titin - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision
C;Accession: I38346
                                                                      A; Status: preliminary; translated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAPKELA 535
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                EMBL: X90569;
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                NID: g1017426;
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Pred. No. 7.
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                                                                                                                            muscle
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hes 252;
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              PIDN: CAA62189.1;
                                                                                                                            ultrastructure
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            PID: g1017427
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A;Gene: GDB:TTN A;Cross-references:

GDB:127867;

OMIM: 188840

A; Map position: 2q31-2q31

A; map	T ROd d	rton: zepz - zepz	
Que Bes Mat	ry Ma t Loc ches	<pre>atch</pre>	š 60;
Qy	10	KKKPTPKPPVVDEAGSGLDNGDFKVT	Ō
Ъ	5837	KKAPPPPKVIKKPVIEKIEKTSRRMEEEKVQVTKVPEVSKKIVPQKPSRTPVQEEVIEVK 5	896
Qу	51 5897	-PKITTAKPINPRPSLPPNSDTSKETSLTVNKETTVETKETTTTNKQTSTDGKEKTT 1 : : : : : : : : :	.06
Qy	107	SIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEP	.61
Db	5950	-VPEEKKPVPVPKKEP	8008
Qy	162	KEPTPTTIKSAPTTPKEPAPTTTKSAPTTPKEPAPTT	206
Db	6009	EEKIPVPVAKKKEAPPAKVPEVQKGVVTEEKITIVTQREESPPP	064
Qy	207	KEPAPTTTKSAPTTPKEPAPTTPKEPAPTTP-KEPAPTTPKEPTPTT-	6
Ф	6065	EIPKKKVPEERK-PVPRKEEEVPPPPKVPALPKKPVPEEKVAVPV	5121
Qy	265	- P 2	265
В	6122	VSKKTVVEEKRFVAEEKLSFAVPQRVEVTRHEVSAEEEWSYSEEEEGVSISVYREEEREE 6	5181
Qy	266	EPAPTK	284
망	6182	PAEVTERQEKKIVLKPKIP	5241
ОУ	285	PTTPKEP-APTTTKEPSPTTPKEPAPT	26
DЬ	6242	.PKKIVPEKNVPAPVPXKEKVPPPNVPEEPXNTVPEANVPFAVIAMBBFBFANV	Ĺ
Qy	327	TKSAPTTPKEPSPTTTKEPAPTT	σ
Вb	6302	KKEAPPKARVPEEPKRAVPEEKVLKLKPKREEEPP	5361
Qy	366		371
Ъ	6362	QPIKEV	5421
Qy	372	PKEPAPTTP	399
Ъ	6422	PEKPIPVKPVPEEPVPTKPKAPPAKVLK	6481
Qy	400	TAPKEPAPTTPKETAPTTPKKLTPTTPEKL	452
дь	6482	VP-EEKVPVP-IPKKLKPPPPKVPEEPKKVFEEKIHISITKREKEQVTEPAAK	6534
Qy	453	PEEPAPTTPKAAAPNTPKEPAPTTPKEPA	490
Db	6535	KEVAPPVRVPEVPKELEPEEVAFEEEVVTHVEEYLVEEEEEY	6594
Qу	491	PTTPKEPAPTTPKGTAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTS	544
Db	6595	EEEVVPVIPVK-VPEVPRKPVPEE-KKPVPVPKKKEAPPAKVPEVPKKPEE	6652
Qy	545	KPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPK	596
Ф	6653	PPAKVPEVPKKPVP-EEKVPVPVPKKVEAPPAKVPEVPK	6702
Qy	597	PAPKELAPTTTKGPTSTTSDKPAPTTPKETAPT-TPKEPAPTTPKKPAPTTP	648
Ъ	6703	EEKKPTPVPKKVEAPPPKVPKKREPVPV	6762
Qy	649	ETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAAT	708

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hypothetical protein At2g27380 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Cacession: C84672 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. R;Lin, X.; Kaul, S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
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A; Map position: 2
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A; Residues: 1-761 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487
A;Accession: C84672
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                                      Qy
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6973
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                                                                                                                                                                           242
                                                                                                                                                                                                                                                              182 PPIKPPVHKPPTPIYSPPIKPPPVHKPPTPIYSPPIKPPPVHKPPTPTYSPPVKPPPVHK
                                                                                                                                                                                                                                                                                                         240
                                                                                                                                                                                                                                                                                                                                                  129 YSPPIYP----PPIQKPPTPSYSPPVKPPPV---QMPPTPTYSPPIKPPPVHKPPTPTYS 181
                                                                                                                                                                                                                                                                                                                                                                              188 KSAPTTPKEPAPTTTKEPAPTTTKEPAPTTTKEPAPTTTKSAPTTP----KEPAPT-- 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 PTPKAETTTKGPALTTP----KEPTPT-TPKEPASTTPKEPTPTTIKSAPTTPKEPAPTTT 187
                                                                                      302
                                                                                                                                                                                                                                                                                                                                                                                                                                         69 PPPIQKPTYSPPIYAPPTYSPPIYSPPIQKPPTYSPPIYAPPIQAPPTY 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KAPKKPTSTKK-----PKTMPRVRK---PKT-TPTPRKMTSTMPELNPTSRIAEAMLQTT 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VPEVPKKVE--EKRIILPK----EEEVLPVEVTEEPEE-----EPISEE 6914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QUTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQKPT 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EEEYVPEEEEFVPEEEVLPEVKPKVPVPAP-----VPEIKKKVTEKKVVIPKKEEAPPAK 6876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KPEMTTTAKDKTTERDL -- RTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTSTTT 766
                                         PAP--TAPKEPAPT----TPKETAPTTP----KKLTPTTPEKLAPTTPEKPAPTT---PE
                                                                                    VKSPPVQKPPTPTYSPP1KPPPVQKPPTPTYSPPIKPPPVKPPTPIYSPPVKP-PPVHKP
                                                                                                             APTTPKEPSPTTTKEP---APTTPKEPAPT--TPKKPAPTTPKEPAPTTTKK 400
                                                                                                                                                                         PPTPIYSPPIKPPPVHKPPTPIYSPPVKPPPVQTPPTPIYSPPVKPPPVHKPPTPTYSPP 301
                                                                                                                                                                                                                  KPAPT-TPKEPAPTTPKEPAP---TTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKS 345
                                                                                                                                                                                                                                                                                           TPKKP---APTTPKEPAPTTP----KEPTP--TTPKEPAPTTKEPAPT-TPKEPAPTAPK 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PMLSDETNICNGKPVDGLTTLRNGTLVAFR 967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VQKKEAPPAKVPEV-
  PTPIYSPPVKPPPVHKPPTPIYSPPVKPPPIQKPPTPTYSPPIKPPPLQKPPTPTYSPPI 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.7%;
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Pred. No. 1.3e-20;
,4; Mismatches 354;
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A; Nolecule type: DNA
A; Rolecule type: DNA
A; Residues: 1-3507 <FAV>
A; Rosidues: 1-3507 <FAV>
A; Cross-references: EMBL:U13646; PIDN:AAC24418.1; GSPDB:GN00021; CESP:ZK783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession. C. Ravello, A.; Vaudin, M. Submitted to the EMBL Data Library, August 1994 Submitted to the sequence of C. elegans cosmid
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A; Reference number: Z21536
A; Accession: T34513
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A; Introns: 14/1; 48/2;
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Best Local Similarity
Matches 252; Conser
                                          2179
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       287
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                                                                                                                                                                                                                                                                                                                                 KKOPNREKIEIDEENSSSSNSGOEKPTTKGIVSSTSATSSESTTAEPHVTTSISSTTSTK
                                                                                                        TVLSSEAPVTSTSPTEVHT-SSETKPSLSASSTTGDTNSTTPSTSSLASVKSTSAPEGTS
                                                                                                                                                                                                                                                                                                                                                                KKKPTPKPPVVDEAGSGLDN-GDFKVTT----PDTSTTQHNKVSTSPKITTA-----K 57
APKKPAPTTPKEPAPTTPKEPAPTTTKEPSPTTP---KEPAPTTTKSAPTTTKEPAPTTTK
                                    ASVAPVKLSSLSPDVSQPSTKTFDATESSTVQASETSSGTSVKSTSEPESHVTKLSITSS
                                                                                                                                                                                                                                                         DMTSSKS-PENVTMSSESPEVSTSSSKSTTASETTVSSTPSESSSSEAPLTSSPATTTEV
                                                                                                                                                                                                                                                                                 PINPRPSLPPN---SDTSKETSLTVNKETTV-ETKETTTTNKQTSTDGKEKTTSAKETQS 113
                                                                       APTTPKEPAPTTPKKPAPTTPK-EPAPTTPKEPTPTTPKEPAPTTKEP-APTTPKEPAPT
                                                                                                                                             TTIKS-APTTPKEPAPTTTKSAPTTPKEPAPTTTKEPAPTTPKEPAPTTTKEPAPTTTKS
                                                                                                                                                                                  ITESSVKSTTPKEESSSEITVKLSSKSPEVTESSVKSSPSTPS-TTSQSVTSTVPETSKS
                                                                                                                                                                                                                   IEKTSAKDLAP----TSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTP 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APKMTKETATTTEKTTESKITATTTQVTSTTTQDTTP 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KPAPTTPKETAPTTPKEPAPTTPKKPAPT-TPETPPPTTSEVSTPTTIK--EPTTIHKSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DESTPELSAEPTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                          11.6%;
                                                                                                                                                                                                                                                                                                                                                                                                       158; Mismatches 416;
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 629; DB 2; Pred. No. 7.2e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     381/1; 586/1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 3507;
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A; Gene: xNopp180
C; Superfamily: nucleolus-cytoplasm
C; Keywords: phosphoprotein
                                                   C; Genetics:
                                                                  A; Molecule type: mRNA
A; Residues: 1-990 <CAI>
A; Cross-references: EMBL: X88927;
                                                                                                                                                                                                                          nucleolar phosphoprotein - African clawed frog C;Species: Xenopus laevis (African clawed frog) C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 C;Accession: I51618; S57757
                                                                                                                                                      A; Title: Identification and cDNA cloning A; Reference number: I51618; MUID:96019267
                                                                                                                                                                                              R;Cairns, C.; McStay, B.
J. Cell Sci. 108, 3339-3347,
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10	754 ITATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTLTTTEIMNKPEETA-KPKD 8:	Qу
35 35	694 PKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMIKETATTTEKTTESK 7.9	Db Qy
93 82	636 APTTPKK-PAPTTPETPPPTTSEVSTPTTTKE-PTTIHKSPDESTPELSAEPTPKALENS 69	Оу
35 22	586 TLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEP 6: :	Оу
6 85	528 KPAPKELAPTITKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPT 58	Qу
27 11	473 AAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTP-KGTAPTTLKEPAPTTPK 52	Оу
72 58	419PTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPAPTTPEEPAPTTP-KA 47 :: ::	Оу
18 14	371PITPKKPAPTIPKEPAPT-TPKEPAPTITKKPAPTAPKEPA-PITPKETA 418	Оу
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42	3 DNKKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPR 62	Qу
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

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100059 segs, 36664827 residues

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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424 7.8 1251 1 YQU3_CAEEL 422.5 7.8 1794 1 YAV1_SCHPO 422.5 7.8 3421 1 TEGU_HSYEB 419.5 7.7 2476 1 ZAN_PIG 419.5 7.7 2476 1 ZAN_PIG 419.5 7.7 185 1 DRPL_HUMAN 419.5 7.7 1291 N121_HUMAN 419.5 7.7 1292 1 N121_HUMAN 419.5 7.6 907 1 VGP3_EBV 411.5 7.6 907 1 VGP3_EBV 411.5 7.6 907 1 VGP3_EBV 407.5 7.5 3256 1 KI67_HUMAN 405.5 7.5 3256 1 KI67_HUMAN 405.5 7.5 3251 1 TCOF_HUMAN 406.5 7.5 3251 1 TCOF_HUMAN 407.5 7.5 3251 1 TCOF_HUMAN 407.5 7.5 3251 1 TCOF_HUMAN 408.5 7.5 3251 1 TCOF_HUMAN
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ALIGNMENTS

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Molecular cloning of human intestinal mucin (MUC2) CONA. Identification of the amino terminus and overall sequence similarity to preprovon willebrand factor."; J. Biol. Chem. 269:2440-2446(1994). ESQUENCE OF 626-1895 AND 4196-5179 FROM N.A. TISSUE-Colon; SEQUENCE OF 626-1895 AND 4196-5179 FROM N.A. MEDILINE-93016075; PubMed-1400449; Gum J.R. Jr., Hicks J.W., Toribara N.W., Rothe EM., Lagace R.E., Kim Y.S.; The human MUC2 intestinal mucin has cysteine-rich subdomains located both upstream and downstream of its central repetitive region."; J. Biol. Chem. 267:21375-21383(1992). [3] SEQUENCE OF 1343-1895 AND 4176-4195 FROM N.A. MEDILINE-93358717; PubMed-1885763; TORIBARA N.W., Gum J.R. Jr., Culhane P.J., Lagace R.E., Hicks J.W., Petersen G.M., Kim Y.S.; MEDILINE-93358717; PubMed-1885763; TORIDATA N.W., Gum J.R. Jr., Culhane P.J., Lagace R.E., Hicks J.W., Petersen G.M., Kim Y.S.; MICC2 human small intestinal mucin gene structure. Repeated arrays and polymorphism "; J. Clin. Invest. 88:1005-1013(1991). 1. FUNCTION: COATS THE EPITHELIA OF THE INTESTINES, AIRWAYS, AND FONCETIVE. LUBRICATING BARRIER AGAINST PARTICLES AND INFECTIOUS ACENTS AT MUCOSAL SURFACES. 1. SUBURIT: MULTIMERIC. 1. SUBCELLULAR LOCATION: SECRETED. 1. TISSUE SPECIFICITY: COLON, SMALL INTESTINE, COLONIC TUMORS, PRONCHUS, CERVIX AND GALL BLADDER. 1. PTM: ALL CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN OR INTEGRAL DEPOTED RESIDED ARE SIMILARITY). 1. POLYMORPHISM: THE NUMBER OF REPEATS IS HIGHLY POLYMORPHIC AND VARIES AMONG DIFFERENT ALLELES. 1. SIMILARITY: CONTAINS 2 VAFC DOMAINS. 1. SIMILARITY: COLONIANS. 1. SIMILARITY: COLONIANS. 1. CTERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).	HUMAN MUC2_HUMAN STANDARD; PRT; 5179 AA. Q02817; Q14878; Q1-JUN-1994 (Rel. 29, Created) Q1-JUN-1997 (Rel. 35, Last sequence update) Q1-NOV-1997 (Rel. 35, Last sequence update) Q1-AUG-2001 (Rel. 40, Last annotation update) MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2). MUC2 QR SMUC. HOmo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606; [1] SEQUENCE FROM N.A. TISSUE-Intestine; MEDLINE-94132002; PubMed-8300571; MEDLINE-94132002; PubMed-8300571; Gum J. R. IT. HICKS I W. Toribara N. W. Siddiki B. Kim V. Gum J. R. IT. HICKS I W. Toribara N. W. Siddiki B. Kim V. Gum J. R. IT. HICKS I W. Toribara N. W. Siddiki B. Kim V. Gum J. R. IT. HICKS I W. Toribara N. W. Siddiki B. Kim V. Gum J. R. IT. HICKS I W. Toribara N. W. Siddiki B. Kim V. Gum J. R. IT. HICKS I W. Toribara N. W. Siddiki B. Kim V.

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PRINTS; PRO0438; GFCYSKNOT.
SMART; SM00211; VWC; 2.
SMART; SM00011; VWC; 4.
SMART; SM00011; VWD; 4.
PROSITE; PS00022; EGF_1; UNKNOWN_1.
PROSITE; PS00125; CTCK_1; 1.
PROSITE; PS01125; CTCK_2; 1.
PROSITE; PS01126; VWFC; 2.
GlyCoprotein; Repeat; Signal.
SIGNAL
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EMBL; M94131;
EMBL; M94132;
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Pfam; PF00395; SLH; 3
PROSITE; PS01072; SLH
                                                                                                                                                        -!- SIMILARITY: CONTAINS 4 S-LAYER HOMOLOGY (SLH) DOMAINS.
                                                                                                                                                                                                                                                           STRAIN-NCIB 10682;
MEDLINE-93209931; PubMed-8458832;
                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes;
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Q06852;
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                                    EMBL; X67506; CAA47841.1;
                                                                                                                                                                                                                                                                                     SEQUENCE FROM
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(Rel. 29, Last sequence update)
(Rel. 33, Last annotation update
E GLYCOPROTEIN 1 PRECURSOR (OUTE
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SLH_DOMAIN;
                       SLH.
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                                                                                                                                                             VVIQPAPIKAASDEPIPTDTPSDEPTPS----
  SETPEEPTPTTTP---
                    TKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTS--
                                                          QDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQ-KP
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T-P-S-D-E-P.
GLY/PRO/SER/THR-RICH.
SLH 1 (INCOMPLETE).
SLH 2.
SLH 3.
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POTENTIAL.
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Pred. No. 5e-31;
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4 X 156 AA APPROXIMATE REF
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5F396695BA9FE74B CRC64;
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P08640; P080
01-AUG-1988
                                                                       Signal;
SIGNAL
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01-FEB-1995 (Rel. 31, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN
GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).
STA1 OR STA2 OR MAL5 OR YIR019C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D., Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D., Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V., Walsh S.V., Whitehead S., Walsh S.V., Whitehead S., Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Saccharomycetaceae; SaccharomycBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=SPX101-1C;
MEDLINE=89031230;
                                                                                                                                                                                                                                             EMBL; Z38061; CAA86176.1;
EMBL; M16164; AAA35014.1;
EMBL; M16165; AAA35015.1;
EMBL; X13857; CAA32069.1;
                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=87194600;
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                         DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Gene fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamashita I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLUCOSE RESIDUES SUCCESSIVELY FROM NON-REWITH RELEASE OF BETA-D-GLUCOSE.
SIMILARITY: TO S. POMBE SPEC15.13.
SIMILARITY: SOME, TO S. POMBE SPCC285.13C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 n Saccharomyces cerevisiae.";
S Lett. 239:179-184(1988).
CATALYTIC ACTIVITY: HYDROLYSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    European
                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboratic sen the Swiss Institute of Bioinformatics and the EMBL outstation burdean Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no was by non-profit institutions.
                                                                                                                                                 S0001458; MUC1.
                                                                                                                                                                           S48478;
                                                                                                                                                                                               A26877;
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; Multigene family.

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YD 817 817
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                                                                                                                        Glycosidase;
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A26877.
S48478.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   600; PubMed=3106330;
Nakamura M., Fukui S.;
is a possible mechanism underlying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AB972;
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                                                                                                                          Polysaccharide
POTENTIAL.
GLUCOAMYLASE S1/S2.
SER/THR-RICH.
N-LINKED (GLCNAC.
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regions
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                                                                                                                          degradation;
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MW; 91C00E2DBD61AA9D CRC64;
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                               NSAGETTSGCSPKTVTTTVPCST
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SEQUENCE FINAL TISSUE-Breast carcinoma;
MEDLINE-90276414; PubMed-2112460;
Hareuveni M., Tsarfaty I., Zarets
9-1han S., Weiss M., Green S., La
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-91097524; PubMed-2268309;
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"172-172-1720-1720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Breast carcinoma;

MEDLINE-90368715; PubMed-1697589;

Gendler S.J., Lancaster C.A., Taylor-Papadimitriou J., Duhio Gendler S.J., Pemberton L., Lalani E.-N., Wilson D. Peat N., Burchell J., Pemberton L., Lalani E.-N., Wilson D. Molecular cloning and expression of human tumor-associated polymorphic epithelial mucin.";
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MEDLINE-90368716; PubMed-2394722;
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"Cloning and sequencing of a human pancreatic
J. Biol. Chem. 265:15294-15299(1990).
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P15941; P15942; P15931; P17626; Q14128; Q16442; Q16437; Q9Y4J2;

Q1-JAN-1990 (Rel. 13, Created)
Q1-APR-1990 (Rel. 14, Last sequence update)
Q1-APR-1990 (Rel. 40, Last sequence update)
MUCIN 1 PRECURSOR (POLYMORPHIC EPITHELIAL MEDIALIN) (PEM) (PEMT)
(EDISIALIN) (TUMOR-ASSOCIATED MUCIN) (CARCINOMA-ASSOCIATED MUCIN)
(TUMOR-ASSOCIATED EPITHELIAL MEMBRANE ANTIGEN) (EMA) (H23AG) (PEANU REACTIVE URINARY MUCIN) (BUM) (BREAST CARCINOMA-ASSOCIATED ANTIGEN)
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MEDLINE-90276413; PubMed=2351132;
Wreschener D.H., Hareuveni M., Tsa
Horov J., Zaretsky J., Kotkes P.,
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Ligtenberg M.J.L., Vos H.L., Gennissen A.M.C.,
"Episialin, a carcinoma-associated mucin, is genolymorphic gene encoding splice variants with
                                                                                                                        SEQUENCE FROM N.A.
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Mammalia; Eutheria;
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Primates;
           Zaretsky J.,
S., Lathe R.,
                                                                                                                                                                                                                                                                                  Tsarfaty
P., Weiss
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                                                                                                                                                                                                                                                                                                                                                                                                                                               173:1019-1029(1990).
                                                                                                                                                                                                                            cDNA sequences. Differential splicing
                                                                                                                                                                                                                                                                               χ.;
                                  Kotkes P., Horev
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י, is generated b
s with alter
           Keydar
                                                                                                                                                                                                                                                                               Smorodinsky N.,
Lathe R., Dion
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Jenerated by a
n alternative
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tumor mucin cDNA.";
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           Wreschner
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This SWISS-PROT entry is copyright. It is produced through a copyred the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Breast carcinoma;
Buluwela L., Liu Q., Luq
Submitted (OCT-1992) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96183746; PubMed=8608966; Weiss M., Baruch A., Keydar I., Wreschner D.H.; Weiss M., Baruch A., Keydar I., Wreschner Callary catranscriptase polymerase chain reaction of the Int. J. Cancer 66:55-59(1996).
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tissue.
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'nocology for the property of the p
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"Sequence analysis of the 5' region
carcinoma-associated antigen gene."
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MEDLINE=96183746;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=91033045; PubMed=1688329;
Tsarfaty I., Hareuveni M., Horev J., Zaretsky J., Weiss M.,
Jeltsch J.M., Garnier J.M., Lathe R., Keydar I., Wreschner D.H.;
"Isolation and characterization of an expressed hypervariable generating for a breast cancer-associated antigen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochem. Biophys.
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POLYMORPHISM:
VARIES FROM 21
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                                                                                                                                                                                                                                                                                          POLYMORPHISM: THE NUMBER OF REPEATS IS HIGHLY POLYMORPHIC. VARIES FROM 21 TO 125 IN THE NORTHERN EUROPEAN POPULATION. MOST PREQUENT ALLELES CONTAINS 41 AND 85 REPEATS. SIMILARITY: CONTAINS 1 SEA DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE SPECIFICITY: ABERRANTLY EXPRESSED TUMORS, SUCH AS BREAST CANCER.
PTM: HIGHLY GLYCOSYLATED (N-AND O-LINKED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lugmani Y.A., Gomm J.J., Coombes R to the EMBL/GenBank/DDBJ databases OR INDIRECT INTERACTION WITH ACTIN
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J05581; AAA59876.1;

K61170; AAB53150.1;

K52229; CAA36478.1;

K52228; CAA36477.1;

K3228; CAA36972.1;

K35293; AAB59612.1;

K35293; AAA5977.1;

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SAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVT
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FLQIYKOGGFL -
ISOFORM).

MISSING (IN 9
T -> A (IN R)
P -> Q (IN R)
A -> T (IN R)
MW; 5E28DFC4
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Pred. No. 1.3e
72; Mismatches
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CYTOPLASMIC (POTENTIAL)
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O (IN REF. 9)
O (IN REF. 9)
O (IN REF. 3)
T (IN REF. 3)
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RESULT 5

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1_MYTED
, FP1_MYTED
, Q25460;
C Q25460;
JT 30-MAY-2000 (Rel. 39, Created)
JT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 20-Aug-2001 (Rel. 40, Last annotation update)
DE ADHESIVE PLAQUE MATRIX PROTEIN (POLYPHENOLIC AD)
PROTEIN 1) (MEFP1) (FRAGMENT).

ADHESIVE

PROTEIN)

RN OCC

Mytilus edulis (Blue mussel). Eukaryota; Metazoa; Mollusca; E Mytiloidea; Mytilidae; Mytilus NCBI_TaxID=6550;

Pteriomorphia;

Mytiloida;

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                           SDETNICNGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSPPS
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HNVTSASGSASGSASTLVHNGTSARATTTPASKSTPFSIPS
                                                                                                              P--GSTAPPAHGVTSAPDTRP---APGSTAPPAHGVTSAPDTRPA
                                                                                                                                                                                                                                                      TTTAKDKTTERDLRTTPETT-----TAAPKMTKETATTTEKTTESKITATTTQVTSTT
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                                                                                                                                         POKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPN
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUSSEL, WYLLUS GGULIS L.";

J. BIOL. Chem. 258:2911-2915(1983).

-!- FUNCTION: PROVIDES ADHESIVENESS TO THE MUSSEL'S FOOT. MUSSELS PRODUCE ONE OF THE STRONGEST WATER INSOLUBLE GLUE. THE MUSSEL'S ADHESIVE IS A BUNDLE OF THREADS, CALLED A BYSSUS, FORMED BY A FIBROUS COLLAGENOUS CORE COATED WITH ADHESIVE PROTEINS.

-!- SUBCELLULAR LOCATION: SECRETED.

-!- SUBCELLULAR LOCATION: SECRETED.

-!- TISSUE SPECIFICITY: PRODUCED BY THE BYSSAL GLAND.

-!- TISSUE SPECIFICITY: PRODUCED BY THE BYSSAL GLAND.

-!- DOMAIN: ALMOST EXCLUSIVELY COMPOSED OF REPEATS OF A DECAPEPTIDE.

-!- PTM: THE DECAPEPTIDE A-K-P-S-Y-P-P-T-Y-K IS POST-TRANSLATIONALLY MODIFIED AS FOLLOWING: THE SIXTH AND SEVENTH RESIDUES ARE HYDROXYLATED AND THE PENULTIMATE IS A 3,4-DIHYDROXYPHENYLALANINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long a
modified and this statement is not removed.
entitles requires a license agreement (See I
or send an email to license@isb-sib.ch).
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InterPro; IPR002965; P_rich_extensn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
MEDLINE-91025829;
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ween the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
                KPA--PTTPKEPA--PTTPKEPA--PTTTKEPA--PTTPKEPA-PTTTKSAPTTTKEPA-
                                                                              PKKPA--PTTPKEPA--PTTPKEPT--PTTPKEP---APTTKEPAPTTPKEPA--PTAPK
KPSYPPTYKAKPSYPPTYKAKPSYPPTYKAKPSYPPTYKAKPSYPPTYKAKPTYKAKPTY
                                                            KAKPSYPPTYKAKPSYPPTYKAKPSYPPTYKAKPTYKAKPTYKAKPTYKAKPSYPPTYKA
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Lee S.M., Link R.P., Sti
nd functional repetition
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decapeptide in the adhesive
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Pred. No. 5.2e-16;
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ion in a marine mussel adhesive
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RESULT 6
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Q9Y493; 000218;
20-AUG-2001 (Rel. 40, 0
20-AUG-2001 (Rel. 40, 1
20-AUG-2001 (Rel. 40, 1
20-AUG-2001 (FRAGMENT).
Gao Z., Harumi T., Garbers D.L.;
"Chromosome localization of the mouse zona zonadhesin gene (ZAN).";
Genomics 41:119-122(1997).
-!- FUNCTION: BINDS IN A SPECIES-SPECIFIC
                                                                                                                                                                                                           "Large-scale sequencing of two analysis of 650 kb of genomic: reveals 17 genes."; Genome Res. 8:1060-1073(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                      MEDLINE=97271566; PubMed=9126492;
                                                                                                                                                                                                                                                                                                                                  Glockner G.,
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                                                                                                                                                                       SEQUENCE OF
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OF THE EGG. MAY BE INVOLVED IN GAMETE RECOGNITION AND/OR SIGNALING.
SUBUNIT: PROBABLY FORMS COVALENT OLIGOMERS.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN, EXCLUSIVEI APICAL REGION OF THE SPERM HEAD (BY SIMILARITY).
TISSUE SPECIFICITY: IN TESTIS; PRIMARILY IN HAPLOID SPERN DOMAIN: THE MAM DOMAINS PROBABLY MEDIATE SPERM ADHESION T

EXCLUSIVELY ON

SPERMATIDS

THE

TRACTS, TO

ZONA PELLUCIDA.

ZONA PELLUCIDA.

DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS DOMAIN: LIKE DOMAIN MIGRT INHIBIT INAPPROPRIATE TRAEPING OF THE MUCIU. LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAEPING OF SPERMATOZOA OR PROMOTING ADHESION TO THE OVIDUCTAL ISTHMUS.

DOMAIN: THE VWFD DOMAINS 2 AND 3 MAY MEDIATE COVALENT OLIGOMERIZATION (BY SIMILARITY TO HUMAN INTESTINAL MUCIN MUC2).

SIMILARITY: CONTAINS 3.5 MAN DOMAINS.

Length

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PRINTS; PRO1217; PRICHEXTE SMART; SM00137; MAM; 2. SMART; SM00014; VWC; 1. SMART; SM00011; VWC_def; 3 SMART; SM00016; VWD; 3. PROSITE; PS01186; EFG_2; 3 PROSITE; PS01186; MAM_1; 1 PROSITE; PS00106; MAM_1; 1 PROSITE; PS00060; MAM_2; 4
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MIM; 602372; -:
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); IPR002919; TIL.
); IPR003328; TILA.
); IPR001007; VWFC.
); IPR001846; Vwd.
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MAM 4.

66. X HEPTAPEPTIDE REPEATS (AUGIN-LIKE DOMAIN).

VWFD 1 (PARTIAL).

VWFD 2.

VWFD 3.

VWFD 4.

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01-JAN-1990 (Rel. 13
01-MAR-1992 (Rel. 21
EXTENSIN PRECURSOR (
"Specific expression of a novel cell wall hydroxyproline-rich glycoprotein gene in lateral root initiation."; Genes Dev. 3:1639-1646(1989).
                                                                          SEQUENCE FROM N.A.
STRAIN-CV. XANTHI; TISSUE-Leaf;
MEDLINE-90188263; PubMed-2612909;
Keller B., Lamb C.J.;
                                                                                                                                                                                                                                 Spermatophyta; Magnoliophyta; eudicotyledons; Asteridae; euasterids I; Solanales; Solanacea
                                                                                                                                                                                                                                                                                       Nicotiana tabacum (Common Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOBAC
                                                                                                                                                                                                          NCBI_TaxID=4097;
                                                                                                                                                                                                                                                                                                                                         HRGPNT3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --EKPTISPEKLTIPTEKPTISTEKPTIPTEKLTIPTEKPTIPTEKPTIPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLKEPAPTTPKKPAPKELAPTTTKEPTSTT----SDKPAPTTPKGTAPTTPKEPAPTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPSPTTTKEPAPTTPKEPAPTTPKKPA-----PTTPKEPAPTTPKEPAPTTTKKPAPTAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TEKPTIPSE-KPTIPSEKPTISTEKPTVPTEE--PTTPTEETTTYMEEPVIPTEKPSIPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PASCKSPRPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPHPSPTA-TGLAALVMSPHAPSTPMTSV---ILGTTTTSRSSTGMSCP-PNARYESCAC
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                                                                                                                                                                                                                                                                                                                                                            (Rel. 13, Created)
(Rel. 13, Last sequence update)
(Rel. 21, Last annotation update)
ECURSOR (CELL WALL HYDROXYPROLINE-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                       tobacco).
Streptophyta;
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No. 1.4
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l.4e-15;
                                                                                                                                                                                                                                                                                       Embryophyta; Tracheophyta;
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                                                                                                                                                                                                                                                                 eudicots;
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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SER-PRO(4). THE PROLINE RESIDUE IS HYDROXYL
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                                                                                                                                                                                                                                                                                                                                                                                             PAPTTPKEPAPTTPKEPAPTTTKEPSPTTPK---EPAPTTTKSAPTTTKEPAPTTTKS---
                                                                                                                                                                                                   APTTPEEPTPTTPEEPAPTTPKAAAP---NTPKEPAPTTPKEPAPTTPKEPAPTTPKETA
                                                                                                                                                                                                                                                                                                                                                                                                                                           P-----PSPSHGHAPPSGGHTPPRGQHPPSHRRPSPPSRHGHPPPTTYAQPPPTPIYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTKSAPTTPKEP-----APTTTKEPAPT---TPKEPAPTTTKEPAPTTTKSAPTTPKE 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AEATTQYGGYLPPPVTSQPPPSSIGLSPPSAPTTTPPSRGHVPSP---RHAPPRHAYPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AETTTK-GPALTTP--KEPTPTT-----PKEPASTTPKE---PTPTTIKSAPTTPKEPAP 184
                                   PPPSPIXSPPPPQVQPLPPTFSPPPPRRIHLPPPPHRQP---RPPTPTYGQPPSPPTFSP
                                                                 APTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKE
                                                                                                    P-----LPPTYSPPPPAYSPPPPPTYSPPPPTYSPPPPAYAQPPPPPPTYSPPPPAYSP
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                                                                                                                                                                                                                                                                                                       RHLPPSPRRQPQPPTYSPPPPAYAQSPQPSPTYSPPPPTYSPPPPSPIYSPPPPAYSPSP
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                                                                                                                                     PTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEP
                                                                                                                                                                   PPPPPSSPPPPSFSPPPPTYEQSPPPPPAYSPPLPAPPTYSPPPPT--YSPPPPTYAQPP
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-TPKKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAE
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H-A-P-P.
2 X 7 AA TANDEM REPEATS OF
1.
2.
CONTAINS THE SER-PRO(4) REFE
CONTAINS THE SER-PROKEN REPE
3 X APPROXIMATE TANDEM REPE
641DD2278AB28524 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 551; DB 1;
Pred. No. 6.6e-16;
4; Mismatches 304
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Carden M.J.;

Continted (MAR-1994) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: I AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALII NF-H HAS AN IMPORTANT FUNCTION IN MATURE AXONS THAT IS NOT SUBSERVED BY THE TWO SMALLER NF PROTEINS.

-!- PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-89089138; PubMed-3145094; Shneidman P.S., Carden M.J., Lees J.F., Lazzarini R.A.; The structure of the largest murine neurofilament protrevealed by CDNA and genomic sequences."; Brain Res. 464:217-231(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NFH_MOUSE STANDARD; PRT; 1087 AA.
P19246; Q61959;
01-NOV-1990 (Rel. 16, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN)
 EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                  use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Mus musculus (Mouse).
                                                                 EMBL;
                                                                                          or send an
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                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Event buropean Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                          PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FU OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY A COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION.
SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                 CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN IN POSITIONS TO 716 AND IS SHORTER DUE TO FRAMESHIFTS.
                                                                                                                                                                                                                                                                                                          PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF. THOUGHT THAT PHOSPHORYLATION OF NFH RESULTS IN THE FORMA INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MA
                                                                                                                                                                                                                                                                                              OF AXONAL CALIBER
M23349;
M24494;
M24495;
M35131;
Z31012;
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                                                                 M24496;
                                                                                                         non-profit institutions as long and this statement is not removed.
                                                                                                        requires
                                                                                          email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                               WEBSTER; TISSUE-Brain;
AAA39813.1;
AAA39813.1;
AAA39813.1;
AAA39809.1;
CAA83229.1;
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subunit.";
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                                                                                                       license agreement
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JT0368; A43778;

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RP--PEQVKSPAKEKAKSPE--KEEAKTSEKVAPKKEEVKSPVKEEVKAKEPPKKVEEEK
                                      TPTTPEE-PAPTTPKAAAPNTPKEPAPTT----PKEPAPTTP----KEPAPTTPKET
                                                                              AKSPVKEDIKPPAEAKSPEKA-KSPVKEGAKPPEKAKPLDVKSPEAQTPVQEEATVPTDI
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27.5%;
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COIL 2B.

COIL 2B.

K -> QA (IN REF. 2 AND 3).

A -> AR (IN REF. 2 AND 3).

S -> T (IN REF. 2 AND 3).

L -> G (IN REF. 2 AND 3).

P -> PREAKSP (IN REF. 3).

MISSING (IN REF. 3).

G -> A (IN REF. 3).

G -> A (IN REF. 3).

T -> N (IN REF. 2 AND 3).

T -> N (IN REF. 2 AND 3).
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50 x 6 AA TANDEM F
GLU/LYS-RICH.
COIL 1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 533; DB Pred. No. 5.3e Nismatches
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COIL 1B.
LINKER 12.
COIL 2A.
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REF. 3).

REF. 3).

"Compared to the state of the sta
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                                                                                                                                                                                                                                                                                  PTTTKSAPTTTKEPAPTT
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P23253;
This SWISS-PROT entry is copyright. It is produced through a copyright the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.
                                                                                                                                                                                                                                        trypomastigotes,";

Trop. Med. Parasitol. 42:146-150(1991).

Trop. Med. Parasitol. 42:146-150(1991).

Trop. Med. Parasitol. 42:146-150(1991).

PARASITE INVASION OF CELLS.

PARASITE INVASION OF CACYLNEURAMINYL OR O-ACYLNEURAMINYL RESIDUES TO GALACTOSE, N-ACETYLHEXOSAMINE, OR N- OR O-ACYLATED NEURAMINYL RESIDUES IN OLIGOSACCHARIDES, GLYCOPROTEINS,

GLYCOLIPIDS OR COLOMINIC ACID.

PARASITE INVASION OR COLOMINIC ACID.

PARASITE INVASION OR COLOMINIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
SIALIDASE (EC 3.2.1.18) (NEURAMINIDASE) (NA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The Trypanosoma cruzi neuraminidase contains bacterial neuraminidases, YWTD repeats of the receptor, and type III modules of fibronecting. Exp. Med. 174:179-191(1991).
                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-91376547; PubMed-1896773;
Prioli R.P., Mejia J.S., Aji T.,
"Trypanosoma cruzi: localization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-SILVIO X-10/4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Euglenozoa; NCBI_TaxID=5693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trypanosoma cruzi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prioli R.P.;
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                                                                                                                                                              DEVELOPMENTAL STAGE: MAXIMAL ACTIVITY IN TRYPOMASTIGOTES, MINIMUM IN EPIVASTIGOTES AND NO DETECTABLE IN AVASTIGOTES.
MISCELLANDOUS: THE VARIABLE LENGTHS OF THE LONG TANDEM REPEAT DOMAIN COULD ACCOUNT IN PART FOR THE POLYMORPHISM OF THE TNCA
                                                                                                                 SIMILARITY:
                                                                                                                                  SIMILARITY:
                                                                                                                                                 PROTEIN
                                                                                                                                                                                                                              (POSSIBLE)
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                                                                                                                FAMILY 33 OF
BNR REPEATS.
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of neur
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                                                                      collaboration
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RESULT 10
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Best Local :
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   CPN_DROME
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CARBOHYD
CARBOHYD
CARBOHYD
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REPEAT
DOMAIN
                                                                             712
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HSSP; P29768; 1DIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M61732; AAA30255.1; PIR; JH0557; JH0557.
                                                                                                                                                                  597
                                                                                                                                                                                                           538
                                                                                                                                                                                                                                 936
                                                                                                                                                                                                                                                                           877
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002860; BNR. Pfam; PF02012; BNR; 2.
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                                                         G,
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                                                                                                                 PTTSEVSTPTTTKEPTTIHKSPDESTP-ELSAEPTPKALENSPKEPGVPTTKTPAATKPE
                                                                                                                                                                                 DSSAH-STPSTPAD-SSAHGTP--STPADSSAHSTP
                                                                                                                                       TP----ADSSAHGTPSTPADSSAHSTPSTPVDSSAHSTPSTPADSS----AHGTPSTPA
                                                                                                                                                        KPAPKELAPTTTKGPTSTTSDKPAPTTPK----ETAPTTPKEPAPTTPKKPAPTTPETPP
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                                                         1127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 9.8%;
Similarity 29.4%;
77; Conservative 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163
209
209
589
342
  STANDARD;
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BNR 1.
BNR 2.
BNR 3.
FIBRONECTIN TYPE-III.
44 X 12 AA TANDEM REPEATS, LTR DOMAIN
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 530.5; DB Pred. No. 7e-15; 0; Mismatches 21
 PRT;
 865
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A
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PKEPAPTTTKSAPTTP-KEPAPTTTKEPAPTTPKEPAPTTTKEPAPT---

TTKSAPTTP

61 233

SPVSAPVAAPVTPSAVAAPVQVVSPAAVAP-----APAAPIAVTPVAPPPTLASVQPAT

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Q
                         Query Match
Best Local Sin
Matches 233;
                                                                                                                                                                                                                                                                                                                                                         Calcium-binding.
CONFLICT 36
CONFLICT 43
CONFLICT 64
CONFLICT 76
CONFLICT 126
CONFLICT 126
CONFLICT 154
CONFLICT 534
CONFLICT 699
CONFLICT 703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazo
Pterygota; Neopte
Ephydroidea; Dros
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q02910;
01-OCT-1993
01-OCT-1993
01-FEB-1994
CALPHOTIN.
CPN OR CAP.
Drosophila m
                                                                                                                                                                                                                   FlyBase;
                                                                                                                                                                                                                             EMBL; L02111; AAA28405.1; -. EMBL; L05080; AAA28420.1; -. PIR; A47282; A47282.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-CANTON-S;
MEDLINE-93165730; PubMed-8434015;
MEDLINE-93165730; PubMed-8434015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-CANTON-S;
MEDLINE-93165729; PubMed-8094559;
Martin J.H., Benzer S., Rudnicka M., Miller C.A.;
"Calphotin: a Drosophila photoreceptor cell calciproc. Natl. Acad. Sci. U.S.A. 90:1531-1535(1993).
       123
APTSKVLAKP-TPK---AETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAPTT 178
                                                                                                                                                                                                                                                                                                                                                    DEVELOPMENT.
                                   Similarity
                                                                                                                                                                                                                   FBgn0010218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          melanogaster (Fruit 1
Metazoa; Arthropoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neoptera;
                        Conservative
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(Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       etazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
eoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Drosophilidae; Drosophila.
                                                                      36
43
64
100
120
127
154
154
150
534
699
721
84781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27, Created)27, Last sequence update)28, Last annotation update)
                                  9.8%;
                                                                                                                                                                                                                   Cpn
                                                                           X.
                        73;
                       Score 530; DB
Pred. No. 5.8e
73; Mismatches
                                                                                   -> L (IN REF. 2).
-> E (IN REF. 2).
2110417E0B0E7CFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fly).
                                                                                 > AVAPAVVA (IN REF. 2).
> T (IN REF. 2).
> V (IN REF. 2).
> A (IN REF. 2).
> AP (IN REF. 2).
> AP (IN REF. 2).
> AP (IN REF. 2).
> T (IN REF. 2).
> L (IN REF. 2).
> L (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                           EARLY IN PHOTORECEPTOR CELL
                                DB 1;
.8e-15;
                        433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.A.;
calcium-binding protein.";
                                                                                                                                                                                              REF.
                                         Length
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                                                                                                                                                                                                                                                                                                                                                                             COMPARTMENT.
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T BINDS 0
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                     Gaps
                     41;
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RESULT 11

FPI_MYTCO STANDARD; PR'
ID FPI_MYTCO STANDARD; PR'
AC Q25434;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 40, Last sequent of the sequ
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                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ADHESIVE PLAQUE MATRIX PROTEIN PRECURSOR (FOOT
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              TISSUE=Foot; MEDLINE=96394686; PubMed=8798340;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAPTTTKEPTSTTSDKPAPTTPKGTAPTTP-----KEPAPTTPKEP--APTTPKGTAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   V----LPPVAAEPVPAVVAEETPETPAPASAPVTIAALDIPEVAPVIAAPSDAPAEAPSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPKEPAPTTPKEPAPTTPKETAPTTP-KGTAPTTLKE-----PAPTTPKKPAPKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPEKL-APTTPEKPAPTTPEELAPTTPEEPTPTTPEEP----APTTPKAAAPNTPKEPAPT 484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVAVAPITAPEPIP----EPEPSLATPTEPIPVEAPVVIQEAVDAVEVPVTETSTSIPET
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J. Mol. Evol. 43:348-356(1996)

J. Mol. Evol. 43:348-356(1996)

PRODUCE ONE OF THE STRONGEST WATER INSCLUBLE GLUE. THE MUSSEL'S PRODUCE ONE OF THREADS, CALLED A BYSSUS, FORMED BY A ADHESTVE IS A BUNDLE OF THREADS, CALLED A BYSSUS, FORMED BY A FIBROUS COLLAGENOUS CORE COATED WITH ADHESIVE PROTEINS.

PIBROUS COLLAGENOUS CORE COATED WITH ADHESIVE PROTEINS.

-!- SUBCELLULAR LOCATION: SECRETED.
-!- TISSUE SPECIFICITY: PRODUCED BY THE BYSSAL GLAND.
-!- TISSUE SPECIFICITY: PRODUCED BY THE BYSSAL GLAND.
-!- TISSUE SPECIFICITY: PRODUCED BY THE BYSSAL GLAND.
-!- PTM: PROLINES IN THE REPEAT ARE HYDROXYLATED (SINGLE OR DI-) AND -!- PTM: PROLINES IN THE REPEAT ARE HYDROXYLATED (SINGLE OR DI-) AND -!- PTM: PROLINES IN THE REPEAT ARE HYDROXYLATED (SINGLE OR DI-) AND -!- PTM: PROLINES IN THE REPEAT ARE HYDROXYLATED (SINGLE OR DI-) AND -!- PTM: PROLINES IN THE REPEAT ARE HYDROXYLATED (SINGLE OR DI-) AND -!- PTM: PROLINES IN THE REPEAT ARE HYDROXYLATED (SINGLE OR DI-) AND -!- PTM: PROLINES IN THE REPEAT ARE HYDROXYLATED (SINGLE OR DI-) AND -!- PTM: PROLINES IN THE REPEAT ARE HYDROXYLATED (SINGLE OR DI-) AND -!- PTM: PROLINES IN THE REPEAT ARE HYDROXYLATED (SINGLE OR DI-) AND -!- PTM: PROLINES IN THE REPEAT ARE HYDROXYLATED (SINGLE OR DI-) AND -!- PTM: PROLINES IN THE REPEAT ARE HYDROXYLATED (SINGLE OR DI-) AND -!- PTM: PROLINES IN THE REPEAT ARE HYDROXYLATED (SINGLE OR DI-) AND -!- PTM: PROLINES IN THE REPEAT ARE HYDROXYLATED (SINGLE OR DI-) AND -!- PTM: PROLINES IN THE REPEAT ARE HYDROXYLATED (SINGLE OR DI-) AND -!- PTM: PROLINES IN THE PROLINES IN 
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InterPro; IPR002965; P_rich_extenso.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VVDEAGSGLDNGDFKVTTPDTST--TQH-----NKVSTSPKITTAKPINPRPSLPPNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YPTKRYQPTYGSKTNYPPIYKPIAKKLSSYKAIKTTYPAYKAKTSYPPSYK-----HKIT 139
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                                                                                                                                                                                                                                                                                                                                                                 PAPTTPKEPAPTT----PKEPTPTT--PKEPAPTTKEPAPTTPKEPAPT-APKKPAPTTP
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                  APTAPKEPAPTTPKETAP ----
                                                                        TYKPKITYPPTYKPKPSYPPSYKPKTYSPTYKPKTTYPPTYKPKPSYPPSYKPKTTYPP
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NONAPEPTIDE 2.
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RESULT 12
MUC1_XENLA
ID MUC1_XENLA
AC Q05049
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"P-domains as shuffled cysteine-rich modules in integumentary muc
T C.1 (FIM-C.1) from Xenopus laevis. Polydispersity and genetic
T polymorphism.";

J. Biol. Chem. 267:24620-24624(1992).

C -!- FUNCTION: COULD BE INVOLVED IN DEFENSE AGAINST MICROBIAL
INFECTIONS. PROTECTS THE EPITHELIA FROM EXTERNAL ENVIRONMENT.

C -!- SUBCELLULAR LOCATION: SECRETED.

C -!- SUBCELLULAR LOCATION: SECRETED.

C -!- ALTERNATIVE PRODUCTS: A NUMBER OF DIFFERENT FORMS OF THE PROJ
C -!- TISSUE SPECIFICITY: SKIN.

C -!- TISSUE SPECIFICITY: SKIN.

C -!- TISSUE SPECIFICITY: SKIN.
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                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Amphibia; Batrachia; Anura; M. Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
INTEGUMENTARY MUCIN C.1 (FIM-C.1) (FRAGMENT).
Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93077556; PubMed=1447205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=8355;
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SIMILARITY: CONTAINS 6 P-TYPE (TREFOIL) DOMAINS.
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12 X APPROXIMATE TANDEM REPEATS,
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Local Similarity

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Score 509.5; DE Pred. No. 3e-14;

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Length

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01-MAR-1992 (Rel. 21, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation updat
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     ; Metazoa;
Eutheria;
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       Chordata;
Primates;
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       Craniata; Vertebrata; Catarrhini; Hominidae;
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Best Local
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EMBL; X74874; CAA52862.1; JU
EMBL; X74873; CAA52862.1; JU
EMBL; X74872; CAA52862.1; JU
EMBL; X74871; CAA52862.1; JU
EMBL; X74870; CAA52862.1; JU
EMBL; X74870; CAA52862.1; JU
EMBL; X74870; CAA52862.1; JU
PIR; S21054; S21054.
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between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wintzerith M., Acker J., Vicaire S., Vigneron M., "Complete sequence of the human RNA polymerase II Nucleic Acids Res. 20:910-910(1992).
                                                                                                                                                                                                                            pfam; pF00623; RNA_pol_A2; 1.

pfam; pF01854; RNA_pol_A2; 1.

pROSITE; pS00115; RNA_pol_A2; 1.

Transferase; DNA-directed RNA polymerase; Transcription; Zinc; DNA-binding; Nuclear protein; Phosphorylation; Zinc-finger.

ZN_FING
71
87
CCH2-TYPE (POTENTIAL).

ZN_FING
1590
1958
CARBOXYL-TERMINAL 7-RESIDUE REPEAT
CONFLICT
1067
1067
W -> L (IN REF. 2).

CONFLICT
1449
1449
1449
D -> Y (IN REF. 2).

SEQUENCE
1970 AA; 217205 MW; 6876FC25692A657E CRC64;
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                                1567
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                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
   263
                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THE PHOSPHORYLATION ACTIVATES POL2.

MISCELLANEOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE III FOR SS AND TRNA GENES.

SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a K., Tsuji H., Morinyo M., Takahashi E., Nenoi M.,
Imura S., Yamauchi M., Hongo E., Hayashi A.;
e human gene encoding the largest subunit of RNA polymerase I
e human gene encoding the largest subunit of RNA polymerase I
e 159:285-286(1995).
FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCH
OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              European Bioinformatics Institute. The by non-profit institutions as long ified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: NUCLEAR. PTM: THE TANDEM 7 RESIDUES REPEATS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNA(N)
                                                                                                                      PTPTTPKEPASTTPKE-PTPTTIKSAPTTPKEPAPTTTKSAPTTPKE-----PAPTTTKE
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 TTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAPTTPKEPAPTTTKEPSPTTPKE
                                PTPGSPGSPGPSSPYIPSPGGAMSPSYSPTSPA-YEPRSPGGYTPQSPSYSPTSPSY-SP
                                                           PAPTTPKEPAPTTTKEPAPTTTKSAPTTPKEPAPTTPKKPAPTTPKEP--APTTPKEPTP
                                                                                           PSPMGGISPAMTPWNQGATPAYGAWSPSVGSGMTPGAAGFSPSAASDASGFSPGYSPAWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                 IPR000684; RNA_polII_repeat.
IPR000722; RNA_pol_A.
IPR002879; RNA_pol_A2.
                                                                                                                                                         Conservative
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                                                                                                                                                      9.3%; Sc
33.3%; Pr
ative 101;
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                                                                                                                                                        Score 503.5;
Pred. No. 1.2e
01; Mismatches
                                                                                                                                                                    503.5;
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1.2e-13;
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P08775;
01-NOV-1988
01-MAR-1992
20-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE-87280135; PubMed-3038894;

Ahearn J.M. Jr., Bartolomel M.S., West M.L.,

"Cloning and sequence analysis of the mouse;
the largest subunit of RNA polymerase II.";
J. Biol. Chem. 262:10695-10705(1987).
                                                                                                                                    Wintzerith M., Acker J., Vicaire S., Vigneron M., Kedinger C., "Complete sequence of the human RNA polymerase II largest subuni Nucleic Acids Res. 20:910-910(1992).

-I- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCIOF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES
                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1587-1970 FROM N.A.
MEDLIND-86068017; PubMed-299785;
Corden J.L., Cadena D.L., Ahearn J.M. Jr., Dahmus I
"A unique structure at the carboxyl terminus of the
of eukaryotic RNA polymerase II.";
proc. Natl. Acad. Sci. U.S.A. 82:7934-7938(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOUSE
                                                                                                                                                                                                                                                                                       REVISIONS, AND PRESENCE OF AN ADDITIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1988 (Rel. 09, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
POLRZA OR RPO2-1 OR RPIIZ15.
                                                                                                                                                                                                                                                                     MEDLINE-92178992; PubMed-1542581;
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     CATALYTIC ACTIVITY: N NUCLEOSIDE TR. RNA(N).
SUBUNIT: RNA POLYMERASE II CONSISTS SUBCELLULAR LOCATION: NUCLEAR.
PTM: THE TANDEM 7 RESIDUES REPEATS (
                                                                                                                              SUBSTRATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDEE 1969
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Best Local
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CONFLICT
SEQUENCE
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or send a
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ZN_FING
71
87
CZH2-TYPE (POTENTIAL).

DOMAIN
1590
1958
CARBOXYL-TERMINAL 7-RESIDUE REPEATS
CONFLICT
1498
1498
P-> R (IN REF. 1 AND 2).

CONFLICT
1499
1536
MISSING (IN REF. 1 AND 2).
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Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                   619
                                                                                               560
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InterPro; IPR000722; RNA_pol_A.
InterPro; IPR002879; RNA_pol_A2.
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MISCELLANEOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE III FOR 5S AND TRNA GENES.
 YSPTSP-TYSPTSPKGSTYSPTSPGY-SPTSP----
                         PAPTTPKETAPTTPKEP--APTTPKKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY
                                                                                                                                             TPKETAPTTPKGTAPTTLKEPAPTTPK-KPAPKELAPTTTKEPTSTTSDKPAPTTPKGTA
                                                                                                                                                                                  PTSP-NYSPTSPSY-SPTSPSY-SPTSP-SYSPSSPR----YTPQSPT-YTPSSPSYSPS
                                                          PTSPTY-SPTTPKY-SPTSP--TYSPTSPYYTPTSPK-----YSPTS---
                                                                            PTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPT-STTSDK
                                                                                                                           SP-SYSPTSPKYT---
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MGI:98086; Rpo2-1
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M14101; AAA40071.1; JOINED
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PF01854; RNA_pol_A2;
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80; Conservative
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                                                                                                                      -PTSPSYSPSSPEYTPASPK--YSPTSPKYSPTSPK-YS
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Pred. No. 2e-1
)1; Mismatches
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MISSING (IN REF. 1 AND 2)
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7D76F38FD92A657E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2e-13
-TYSLTSPAI ---
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В
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-!- FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L.
AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER
NF-H HAS AN IMPORTANT FUNCTION IN MATURE AXONS THAT IS NOT
SUBSERVED BY THE TWO SMALLER NF PROTEINS.

-!- PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P, NFH
PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF. IT IS
THOUGHT THAT PHOSPHORYLATION OF NFH RESULTS IN THE FORMATION OF
INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE
OF AXONAL CALIBER.

-!- PTM: PHOSPHORYLATION SEEMS TO PLAY * '--
OF THE LARGER NEWLY.
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P16884; Q63368;
01-AUG-1990 (Re]
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01-FEB-1994 (Rel. 28, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT
NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H) (FRAGMENT).
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Jolles P.
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                                                                                                                                                                                                                                                                                                                                       Lieberburg I., Spinner N., Snyder S., Anderson J., Goldgaber D., Smulowitz M., Carroll Z., Emanuel B.S., Breitner J., Rubin L., "Cloning of a cDNA encoding the rat high molecular weight neurofilament peptide (NF-H): developmental and tissue expression the rat, and mapping of its human homologue to chromosomes 1 and "2" "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Breen K.C., Robinson P.A., Wion D., Anderton B.H. "Partial sequence of the rat heavy neurofilament Identification of putative phosphorylation sites. FEBS Lett. 241:213-218(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NF-H)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 37-831 FROM N.A.
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                                                                         LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION. SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY. CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION.
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ltu detection.";
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    SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation een the Swiss Institute of Bioinformatics and the EMBL outstation on its
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EMBL; X13804; CAA32038.1
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Patent No. 6071518
                                                                                                                          GENERAL INFORMATION: APPLICANT: Peters
                                                     APPLICANT: Petersen, Carolyn
TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: SPECIES INFECTIONS
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TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 650-324-1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1837 amino acids
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STATE:
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CLASSIFICATION:
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                       782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KVTTPDTSTTQHNKVSTSPKITTAKPINPRPSLPPNSDTSKETSLTVNKETTVETKETTT 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPT 152
                                                                                                                                                                                                                                                                                                                                            TTTATTTTKKPTTTTTTTTTKKPTTTTTATTTTTTSETESVIKPDEWCWLEKNGECE
                                                                                                                                                                                                                                                                                                                                                                         KEPAPTTTKEPAPTTTKSAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKE---
                                                                                                                                                                                                                                                                                                                                                                                                          PTTPKEPASTTPKEPTPTTIKSAPTTPKEP--APTTTKSAPTTPKEPAPTTTKEPAPTTP 210
                                                                                                                                                                                                                 RSLDFTIPPVAGHNSCSIIVGVSGGGKIHVSPYGSKDVSLISAPIQPCELFNEVYCDTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AKYGAIHSGYQTSADEVTTTTAKPTTTTTGAPGQPTTTTTGSPSKPTTTTTKATTTTTI 726
                                                                                                           ----APTITKEPAPTITKSAPTIPKEPSPTITKEPAPTIPKEPAPTIPKEPA 386
                         TTTTKRDEMTTTTPLPDIGDIEITPIPIEKMLDKYTRMIYDYNSGLLLDSNDEPIPGSQ
                                                     PTTPKEPAPTTTKKPAP--
                                                                                   LNPIITTTQKPTTTTTKVPGKPPIATTTTLKPIVTTTTKATTTTTTVPTT-----
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PatentIn Release #1.0
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12-SEP-1997
                                                                                                                                                                     --APTTPKEPAPTT---PKEPAPTTTKEPS-PTTPKEPAPTTTKS- 330
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21.3%; Pred. No. 4.7e-25;
ative 100; Mismatches 494;
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;PATENT NO. 5202236
; APPLICANT: MAUGH, KATHY J.;ANDERSON, DAVID M.;STRAUSBERG,
;SUSAN L.;MCCANDLISS, RUSS;WEI, TENA;FILPULA, DAVID
;SUSAN L.;MCCANDLISS, MUSCHOOD OF PRODUCING BIOADHESIVE
;TILE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
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           NUMBER OF SEQUENCES: 39
CURRENT APPLICATION NOWABER: US/07/528,762
FILING DATE: 25-MAY-1990
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APPLICATION NUMBER: 82,456
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                                                                                                                                                                                                                                                                                    DPQTGEQIKGSVPYVSLYVKEKNIVTEAAYGLPVDPKTGFPIDPISYLPFAKNGELIDPI 1636
                                                                                                                                                                                                                                                                                                                                                                                                                                               TPTPRKMTSTMPELNPTSRIAEAMLQTTTRPNQTPNSKLVEVNPK-SEDA------
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                                                                                                                                                                                                                                SGKYF
                                                                                                                                                                                                                                                                                                                          NPMLSD-----
                                                                                                                                                                                                                                                                                                                                                                                                                MPVPGKPQGENGGIMTPEQILEAL-----NKLPTSNEVNISPRPSSDAVPDRPTNTWW 1518
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APPLICATION NUMBER: 933,945
FILING DATE: 24-NOV-1986
APPLICATION NUMBER: 650,128
FILING DATE: 13-SEP-1984
EQ ID NO:25:
LENGTH: 744
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nes 239; Conserv
                                                        PSYP--PTYKAKPSYPPTYKAKPSYPPTYKAKPTYKAKPTYPSTYKAKPSYPPTHKAKPT
                                                                                    PKEPGVPTTKTPAA-----TKPEMTTTAKDKTTERDLRTTPETTTAAP-----KMT 739
                                                                                                                   YKAKPSYPPTYKAKPSYPPTYKAKPSYPPTYKAKPSYPPTYKAKPTYKAKPTYPSTYKAK
                                                                                                                                                  ---TPETPPPTTSEVSTPTTTKE----PTTIHKSPD----ESTPELSAEPT-PKALENS
                                                                                                                                                                                  PPTYKAKPTYK-AKPTYKAKPTYPSTYKAKPSYSPTYKAKPSYP----PTYKAKPSYPPT
                                                                                                                                                                                                            -PTTPKKPAPKELAPTTTKGPT--STTSDKPAPTTPKETAPTTPKEPAPTTPKKPA--PT
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29.9%; Pred. No. 2.2e-25;
ative 78; Mismatches 308;
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RESULT 4 US-09-103-429A-3

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Best Local Similarity
Matches 200; Conserv
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INFORMATION FOR SEQ ID NO:
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APPLICANT: Wang, Ping
TITLE OF INVENTION: A No. 6187558el Invertebrate Intestinal Mucin
TITLE OF INVENTION: cDNA and Related Products and Methods
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COMPUTER READABLE FORM:
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REFERENCE/DOCKET NUMBER: BT:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (607) 256-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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ORGANISM: Tri
TISSUE TYPE:
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HYPOTHETICAL:
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NAME: Michaels, Christopher A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 PTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAPTTPKEPAPTTTKSAP 191
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OPERATING SYSTEM:
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362 CGAGTHFSFELQQCDHIELVGCTLPGGESEEVDVDEDA-CTGWYCPTEPIEWEPLPNGCP
                                                                                                                                                                                                                                                   242 ELLPNGCPADFDIHLLIPHDKYCNLFYQCSNGYTFEQRCPEGLYFNPYVQRCDSPANVEC
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TYPE: amino acid
STRANDEDNESS: single
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SYSTEM: PC-DOS/MS-DOS
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                                                                  ---KSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKEP
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; Sequence 5, Application US/08700651B
; Patent No. 6015882
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TYPE: PRT
; ORGANISM: Cryptosporidium parvum
US-08-700-651-5
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EARLIER FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 5
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 284; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF CRYPTOSPORIGIUM PARVUM TITLE OF INVENTION: INFECTIONS FILE REFERENCE: 480.19-4(HV) CURRENT APPLICATION NUMBER: US/08/700,651B CURRENT FILING DATE: 1997-08-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NQCTSTAAPTAAPTAAPTAAPTAAPTA--APSTVVPPATPPATAAPVPPTT---AIPT--
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PTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPK 289
                                                                                                                                        ETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTP 169
                                                                                                                                                                            APCNSENSFEQGQIFDMGSKVYIPYTKCVGVKHTTTTTTTTTTTTTTTT--
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                                    TTIKSAPTTPKEPAPTTTKSAPTTPKEPAPTTTKEPAPTTPKEPAPTTTKEPAPTTTKSA 229
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Pred. No. 7.3e-24;
2; Mismatches 476
                                                                                                              -TSLTVNKETTVETKETTTNKQTSTDGKEKTTSAK 109
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IDLETGLPRDPVSGLPQLPNGTLV 1281
                                                          QQTDEITGKPVDTVTGLPYDPSTGEIIDPATKLPIPGSVAGDEILTEVLNITTDEVTGLP 1257
                                                                                           EVTPD------MDYLPRVPNQGIIINP--------MLSDETNICNGK-----
                                                                                                                                                                                                                                                           VYGLPVGEITGLPKDPGSDIPFNSTTGELVDPSTGKPINNSTAGIVSGKPGLPPIEDENG
                                                                                                                                                                                                                                                                                                                            IMKTPTQTDSVTGKPIDPTTGLPFNPPTGHLINPTNNNTMDSSFAGAYKYAVSNGIKTDN 1023
                                                                                                                                                          -----LNPTSRIAEAMLQTTTRPNQTPNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMP
                                                                                                                                                                                                                                                                                             IMNKP--EETAKPKD-----RATNSKATTPKPQKPTKAPKKPTSTKKPKTMP-----
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                                                                                                                                                                                                                                                                                                                                                                                            -PSVP-----ESIPE-----KDQKIDSISELMYDIESGRLIGQVSKRPIPGSIAGDLNP 963
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                                 -PVDGLTTLRNGTLV 964
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 9.0%;
Best Local Similarity 22.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HTELEPHONE: 650-324-1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino a STRANDEDNESS: TOPOLOGY: line
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
          351
                                         290
                                                                            301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Petersen, Carolyn
TITLE OF INVENTION: PETILDS, POLYPEPTIDES, GLYCOPROTEINS,
TITLE OF INVENTION: PETILDS, POLYPEPTIDES, GLYCOPROTEINS,
TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                             241
                                                                                                                                                                               170
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                                                                                                                                                                                                                                                                      159 APCNSENSFEQGQIFDMGSKVYIPYTKCVGVKHTTTTTTTTTTTTTTTTTTTT------
                                                                                                                                                                                                                                                                                                                65 LPPNSDTSKE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/0 FILING DATE: 12-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 94306-1840
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CITY: Palo Alto
STATE: CA
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                                                                 PTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPTPTTPKEPAPTTPKEPAPTTPKEPAPTAPK 289
                                                                                                                                    TTIKSAPTTPKEPAPTTTKSAPTTPKEPAPTTTKEPAPTTTKEPAPTTTKSA 229
                                                                                                                                                                                                                                      ETQSIEKTSAKDLAPTSKYLAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTP 169
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5 Sherman Avenue, Suite 6
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                                                                                                                                                                                                       Score 489; DB 3; Length 1721;
Pred. No. 7.3e-24;
2; Mismatches 476; Indels 44
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RESULT 7
US-07-638-431-2
Sequence 2, Application US/07638431
Patent No. 5198535
GENERAL INFORMATION:
APPLICANT: Hoffman, Stephen L.
APPLICANT: Charoenvit, Yupin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APTTPKEPAPTTPKKPAPTTPETPPPTTSEVSTPT----TTKEPTTIHKS-----
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                                                                                                                                                                        QQTDEITGKPVDTVTGLPYDPSTGEIIDPATKLPIPGSVAGDEILTEVLNITTDEVTGLP 1257
                                                                                                                          IDLETGLPRDPVSGLPQLPNGTLV 1281
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STREET:
CITY: B
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-07-638-431-2
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Best Local Similarity
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INFORMATION FOR SEO ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 826 amino acids
TYPE: AMINO ACID
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APPLICANT: Khusmith, Srisin
APPLICANT: Rogers IV, William O.
TITLE OF INVENTION: Protective malaria sporozoite surface
TITLE OF INVENTION: immunogen and gene
NUMBER OF SEQUENCES: 2
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APPLICATION NUMBER: US
FILING DATE: 19910110
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CLASSIFICATION:
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SOFTWARE: Patentl
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STREET: NMRDC Building 1 T-
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                                     PKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPT
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.2
                                                                                   ---PSNPEEPNPEE---PSNPKEP----SNPEEPINPEELNPKEPSNPEESN
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) 295-4033
) ID NO: 2:
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26.4%; Pred. No. 3.5e-24;
7ative 54; Mismatches 223;
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NPEESNPKEP----INPEDNENPLIIODEPIEPRNDSNVIPI
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; TOPOLOGY: 1:
; MOLECULE TYPE:
PCT-US92-00018-2
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PCT-US92-00018-2
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Best Local
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INFORMATION FOR SEO ID NO: ...
SEQUENCE CHARACTERISTICS:
LENGTH: 826 amino acids
TYPE: AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Spevack, Avram D.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 295-6759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SUFFWARE: Patentin Release #1.2.
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APPLICANT: Hedstrom, Richard
APPLICANT: Khusmith, Srisin
APPLICANT: Rogers IV, William O.
TITLE OF INVENTION: Protective malaria sporozoite surface |
TITLE OF INVENTION: immunogen and gene encoding
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MEDIUM TYPE: Floppy disk
         393
                          444 PNKPNP----NEPSNPNKPNPN-----EPLNPNEPSNPNEPSNPNAPSNPNE--PSNPNE 492
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APPLICANT: Charoenvit, Yupin
APPLICANT: Hedstrom, Richard
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STREET: Medical Center
CITY: Betheads
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                                                                                                                                                                                                                                                                                      Local Similarity
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PAPTTTKKPAPTAPKEP-APTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAP 451
                                                        TKEPAPTTIKSAPTIPKEPSPTTIKEPAPTIPKEPA-PTIPKKP-APTIPKEPAPTIPKE 392
                                                                                    RRNPKRRNPNKPKPNKPNPNKPNPNEPSNPNKPNPN----EPSNPNKPNP----NEPSN 443
                                                                                                         PTTPKEPAPTAPK--KPAPTTPKEPAPTTPKEPAPTTTKSAPTT 334
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Best Local (
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707 PYKGHEERIPKPHRSNDDYVYDNNVNKNNKDEPEIPNNE 745
                                                                                                                                                                                                                                                                                                                   511 KGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTT 570
                                                                                                                                                                                                                                                                                                                                                                                                452 TTPEEPTPTTPEEPAPTTPKAAAPNTPKEP-APTTPKEPAPTTPKEPAPTTPKETAPTTP 510
                                                                                      LPIIPQKGNNIPSNLPENPSDSEVEYPRPNDNGENSNNTMKSKKNI---PNEPIPSPGDN 706
                                                                                                                             TPKEP-----APTTPKKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPDESTPELSAE 684
                                                                                                                                                                                                                          PKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPT
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                                                ----- 703
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RESULT 9
5202236-13
;Patent No. 5202236
; APPLICANT: MAUGH, KATHY J.;ANDERSON, DAVID M.;STRAUSBERG,
;SUSAN L.;MCCANDLISS, RUSS;WEI, TENA;FILPULA, DAVID
;SUSAN L.;MCCANDLISS, RUSS;WEI, TENA;FILPULA, DAVID
;TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE NUMBER OF SEQUENCES: 39
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-MAY-1990
APPLICATION NUMBER: 82,456
FILING DATE: 07-AUG-1987
APPLICATION UMBER: 933,945
FILING DATE: 24-NOV-1986
APPLICATION NUMBER: 650,128 FILING DATE: 13-SEP-1984

/ Match 8.8%; Score 476.5; DB 6; Local Similarity 29.7%; Pred. No. 1.6e-23; nes 221; Conservative 71; Mismatches 284; 71; Indels 169; Length 45;

253 AKPTYKAKPTYKAKPTYPSTYKAKPTYP----PTYKAKPSYPPTYKAKPTYKAKPTYKAK 330 SAPTTTKEPA-----PTTTKSAPTTPKEPSPTTTKEPA--PTTPKEPA----PTTPKK 376 51 PKITTAKPINPRPSLPPNSDTSKETSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKE 110 PTPTTIKSAPT-TPKEPAPTTIKSAPTTPKEPAPTTTKEPAPTTPKEPAPTTTKEPA--P 223 PKMTYPPTYKPKPSYPP------TYKSKPTY-----KPKIT----YP----PTYKAKPSYPPTYKAKPSYPPTYKAKPSYPPTYKAKPSYPSLIKAKPSYPPTYK TPKEPAPTAPKKPA--PTTPKEPA--PTTPKEPAPTTTKEPSPTTP-----KEPAPTTTK 329 PTYKPKPSYP--PSYKTKKTYPPTYKPKLTYPPTYKPKPSYPPSYKPNKTYPPTYKPKLT 196 TTTKSAPTTPKEPAPTTPKKPAPT-TPKEPAPTT----PKEPTPTTPKEPAPTTKEPAPT 278 SYPPTYKSKPTYKPKITYPPTYKAKPSYPPTYKPKKTYPPT-YKPKLTYPPTYKPKASYP ------YPPTYK--AKPS------YPPTYKPKKTYPPTYKPKLTYPPTYKPKP TQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKE----PASTTPKE 166 252 138 40

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                                                                                                                                                                                       ; OTHER INFORMATION:
; OTHER INFORMATION:
US-09-219-849-5
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                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/09219849 Patent No. 6150081
                                                                                                                                                                                                                                                                                                SOFTWARE:
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                                                                                                                   Matches 173;
                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/219,849
CURRENT FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 50
                                                                                                                                                                                                                                                 LENGTH: 960
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                      FEATURE:
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                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPA--PTTPKKP
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                                                                                    PTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAPTTPKEPAP--TTTKS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YPPTHKAKPTYKAKPSYPPTHKAKP
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                          APTTPKEPAPTTTKEPA-PTTPKEPAPTTTKEPAPTTTKSAPTTPKEPAPTTP---KKPA
GPPGSRDPGPPGAPGPAGPPGSRDPGPPGAPGPPGSRDPGPPGAPGPAGPPGSRDPG
                                                           PGPAGPPGSRDPG--PPGAPGPAGP--PGSRDPGPPGAPG-PAGPPGSRDPGPPGAPGPA
                                                                                                                                                                                                                                                                                                               PatentIn Ver.
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VAN RIJN, ALEXIS C.
BOUWSTRA, JAN B.
DE WOLF, FREDERIK A.
                                                                                                                     Conservative
                                                                                                                                                                                                          Description of Artificial Sequence: Illustrative amino acid sequence
                                                                                                                                   8.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GEORGE V.
                                                                                                                       60;
                                                                                                                     score 452; DB 4;
Pred. No. 9.3e-22;
0; Mismatches 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/08479537A Patent No. 5861381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
            PRIOR APPLICATION DATA:
APPLICATION NUMBER: FILING DATE: 23-OCT-
                                                                                                   SOFTWARE: Patentin Relicurrent APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187
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                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: HAREUVENI, Mara
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              331
                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                             CITY: Alexandria
STATE: Virginia
                                                                  FILING DATE: 07
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                          ZIP: 22313-1404
                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGPPGSRDPGPPGAPGPAGPPGSRDPGPPGAPGPAGPPGSRDPGP----PGAPGPAGPPG 404
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APPLICATION
                                                                                                                                                                                                                                            Virginia
United States
                                                                                                                                                                                                                                                                                                P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                          LATHE,
                                                                                                                                                                                                                                                                                                                                                                                                                                       KIENY, Marie-Paule
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAMBON,
                                                                                                                                                                                                                                                                                                                   BURNS, DOANE,
                  23-OCT-1990
                                                                                     07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                          Richard
                                                                                                                                                                                                                                                                                                                                                                       TREATMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pierre
                                                                                                                                                                                                                                                                                                                                                                       PHARMACEUTICAL COMPOSITION FOR THE TREATMENT OR PREVENTION OF A MALIGNANT
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                                   FR 90/13101
                                                                                                         US/08/479,537A
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                                                                                                                                            Version
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NAME/KEY: Peptide
LOCATION: 1..21
COTHER INFORMATION:
OTHER INFORMATION:
US-08-479-537A-5
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Best Local
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 128..172:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
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                                                     218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/403,576
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER

PILTATION NUMBER

PILT
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LOCATION:
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LOCATION: 128..1727
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REGISTRATION NUMBER: 35,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
              TSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKD-LAPTSKVLAKPT 133
                                                                               --DNKPAPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS
                                                                                                                                    TTPKEPAPTTT-----KSAPTTPKEP
                                                                                                                                                                      PGSGSSTTQGQDVTLAPATEPASGSAATWGQDVTSVPVTRPALGSTTPPAHDVT---SAP
                                                                                                                                                                                                                 P-KAETTTKGP--ALTTPKEP------TPTTPKEPASTTPKEPTPTTIKSAP 176
                                                                                                                                                                                                                                                               TVLTV-----VTGSGHASSTPGGEKETSATQRSSVPSSTEKNAVSMTSSVLSSHS
                                                                                                                                                                                                                                                                                                                                                                  Similarity 23.7
55; Conservative
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147
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134
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                                                                                                                                                                                                                                                                                                                                                                                   7.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Amino acids 1 to 21 are a
21 amino acid precursor sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Amino acid 147 is x2 = xaa which is the codon for Pro or Ala wherein or CCG; and Ala = GCT, GCC, GCA, or GCG."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Amino acid 144 is y = Xaa which is the codon for Thr or Asn or ACG; and Asn = AAT or AAC."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Amino acid 134
which is the codon for
or CCG; and Ala = GCT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "The amino acids spanning 128 to 1727 constitute a repeated region wherein the repeat 20 amino acids, 17 of which are fixed. The number of such repeats varies from 1 to 40."
                                                                                                                                                                                                                                                                                                                                                                  69;
                                                                                                                                                                                                                                                                                                                                                           Score 424.5; DB 2;
Pred. No. 1.1e-19;
9; Mismatches 511;
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Pro or Ala wherein Pro = CCT,
GCC, GCA, or GCG."
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                                                                                         RESULT 12
US-09-083-116-5
US-09-083-116-5
: Sequence 5, Application US/09083116
: Patent No. 6203795
: GENERAL INFORMATION:
: APPLICANT: CHAMBON, Pierre
: APPLICANT: KIENY, Marie-Paule
: APPLICANT: HATHE, Richard
: APPLICANT: HATHE, Richard
: APPLICANT: HATHE, Richard
: APPLICANT: HATHE, Richard
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                   TITLE OF INVENTION: PHARMACEUT TITLE OF INVENTION: TREATMENT NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                      VTSAPDXRPXPGSTAPXAHGVTSA------PDXRPXPGSTAPXAHGVTSAPD 1003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DXRPXPGSTAPXAHGVTSAPDXRPXPGST--APXAHGVTSAPDXRPXPGSTAPXAHGVTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - PNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLSD
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       BURNS,
                                                              PHARMACEUTICAL COMPOSITION FOR THE TREATMENT OR PREVENTION OF A MALIG
    DOANE,
  SWECKER
MATHIS,
                                                              MALIGNANT
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OTHER INFORMATION:
OTHER INFORMATION:
US-09-083-116-5
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RELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEPAX: (703) 836-6201
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1667 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: WO PCT/FR91/00835

APPLICATION NUMBER: 23 - OCT - 1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/039,320

FILING DATE: 04 - APR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/403,576

FILING DATE: 14 - MAR-1995

ATTORNEY/AGENT INFORMATION:

NAME: TESTION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:

NAME/KEY: Peptide

134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Peptide
LOCATION: 128..1727
OTHER INFORMATION: /
OTHER INFORMATION: 1
OTHER INFORMATION: 2
OTHER INFORMATION: x
                                                                                                                                                                                                                                     FEATURE:
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CITY: Alexandria
STATE: Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Teskin, Robin L. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION:
OTHER INFORMATION:
                                                                             NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                       OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                     OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                  NAME/KEY: Peptide LOCATION: 147
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                                                                                 Peptide
1..21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "The amino acids spanning 128 to 1727 constitute a repeated region wherein the repeat 20 amino acids, 17 of which are fixed. The number of such repeats varies from 1 to 40."
                                                                                                                                                                                                                                                       /note= "Amino acid 144 is Y = Xaa
which is the codon for Thr or Asn wherein Thr =
or ACG; and Asn = AAT or AAC."
                                                                                                                                                                                                                                                                                                                                                                        /note= "Amino acid 134 is X1 = Xaa which is the codon for Pro or Ala wherein Pro or CCG; and Ala = GCT, GCC, GCA, or GCG."
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                                                                                                                                         /note= "Amino acid 147 is X2 = Xaa
which is the codon for Pro or Ala wherein Pro =
or CCG; and Ala = GCT, GCC, GCA, or GCG."
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                                          /note= "Amino acids 1 to 21 are a 21 amino acid precursor sequence."
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943 ETNICNGKPVDGLTT-LRNGTLVAFRGHYFWMLSPFSPPSPARRITEVWGIPSPID 997	912 APXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPX	884 -PNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLSD 94	869 -GSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSA-PDXRPXPGST	824 KPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPNQT 8	821 APDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXP- 8	764 TTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQ 8	763 DXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS	708 -TKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTS 7	703 DXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAP	662 TTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAA	645 RPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAP	618 KPAPTTPKETAPTTPKEPAPTTPKKPAPTTPETPPPTTSEVSTP	586 PXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAP-XAHGVTSAPDX	572 KEPAPTTPKGTAPTTLKEPAPTTPKRPAPKELAPTTTKGPTSTTSD		PKEPAPTTP	S	σ	4	413 TPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPAPT 468	HGVT		301 APDXRP-XPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVT 359		241 APDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS 300		181 APDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS 240	218 TKEPAPTTTKSAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPIPTT 264	123DNKPAPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS 180			IKSAP	16 TVLTVVTGSGHASSTPGGEKETSATQRSSVPSSTEKNAVSMTSSVLSSHS 65	STDGKEKTTSAKETQSIEKTSAKD-LAPTSKVLAKPT 1	Query Match 7.8%; Score 424.5; DB 4; Length 1867; Best Local Similarity 23.7%; Pred. No. 1.1e-19; Matches 255; Conservative 69; Mismatches 511; Indels 241; Gaps 53

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RESULT 13
US-08-479-537A-2
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                                                                                                                                                                                                                                                                                                                                               TELEFAX: (703) 836-202
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                    FEATURE:
NAME/KEY:
                                                NAME/KEY: Peptide LOCATION: 134
OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                NAME/KEY: Peptide
LOCATION: 128.1899
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/403,576
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/039,320 FILING DATE: 04-APR-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR91/00835
FILING DATE: 23-OCT-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: 1
APPLICANT: 1
                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 514 PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                        EATURE:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 23-OCT
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                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: United States ZIP: 22313-1404
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CITY: Alexandria
STATE: Virginia
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o. 5861381
                                                                                                                                                                                                                                                                                                                                 2035 amino acids
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(703) TD NO: 2:
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                                                                                                                                                                                                                  Peptide
128..1899
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LATHE, Richard
HAREUVENI, Mara
VENTION: PHARMACEUTICAL COMPOSITION
VENTION: TREATMENT OR PREVENTION OF
                                                                                                                                                                                                                                                                                      linear
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                    Peptide
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                                                                                                                                                                                                                                                                    peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-OCT-1990
                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                /note= "The amino acids spanning
128 to 1899 constitute a repeated region wherein the
20 amino acids, 17 of which are fixed. The number of
repeats varies from 1 to 40."
                                           /note= "Amino acid 134 is x1 = xaa
Xaa Xaa which is the codon for Pro or Ala wherein
CCC, CCA, or CCG; and Ala = GCT, GCC, GCA, or GCG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FR 90/13101
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Best Local Similarity
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                                           662
                                                                          645
                                                                                                          618
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OTHER INFORMATION:
OTHER INFORMATION:
          703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 APDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS 300
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LOCATION: 1..21
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            360
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LOCATION:
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OTHER
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OTHER INFO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99
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DXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAP
                                                                RPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGS--TAPXAHGVTSAP
                                                                                                                                PXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAP-XAHGVTSAPDX
                                                                                                                                                               KEPAPTTPKG----TAPTTLKEPAPTTP-----KKPAPKELAPTTTKGPTSTTSD
                                                                                                                                                                                               TAPXAHGVTSAPDXRPXPGSTAP-XAHGVTSAPDXRPXPGSTAPXAHGVTS----APDXR
                                                                                                                                                                                                                                TTP------KKPAPKELAPTTTKEPTSTTSDKPAP--TTPKGTAPTTPKEPAPTTP
                                                                                                                                                                                                                                                                                                TPKA----AAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGT-APTTLKEPAP
                                                                                                                                                                                                                                                                                                                                 SAPDXRPXPGSTAPXAHGVTS----APDXRPXPGSTAPXAHGVTSAPDXRPX----PGST
                                                                                                                                                                                                                                                                                                                                                               TPKETAP----TTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPT
                                 TTTKEPTT----IHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAA-----
                                                                                                                                                                                                                                                                                                                                                                                                 SAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TVLTV------VTGSGHASSTPGGEKETSATORSSVPSSTEKNAVSMTSSVLSSHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --DNKPAPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGSGSSTTQGQDVTLAPATEPASGSAATWGQDVTSVPVTRPALGSTTPPAHDVT---SAP 122
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147
                                                                                                        -ETAPTTPKEPAPTTP--
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23.7%; Pred No. 1.2e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Amino acids 1 to 21 are \epsilon 21 amino acid precursor sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Amino acid 144 is y = Xaa which is the codon for Thr or Asn wherein Thr = or ACG; and Asn = AAT or AAC."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69;
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n for Pro or Ala wherein
GCT, GCC, GCA, or GCG."
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                                                                                                                                                                                                                                                                                                                FILING DATE: 23-OCT-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/039,320

FILING DATE: 04-APR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/403,576

FILING DATE: 14-MAR-1995

ATTORNEY/AGENT INFORMATION:

NAME: TRACE: TRACE: TRACE

NAME: 
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                                                                                       REGISTRATION NUMBER: 017/
REFERENCE/DOCKET NUMBER: 017/
REFERENCE/DOCKET NUMBER: 017/
RELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEPHAX: (703) 836-2021
                            TELEFAX: (703) 836-202:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2035 amino acid
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APPLICANT: HAREUVENI
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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CLASSIFICATION:
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                            NAME: Teskin, Robin L. REGISTRATION NUMBER: 3
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TOPOLOGY: line
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LOCATION:
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                                                                                                                                                                                                                                                                                                           TKE--PAPTTT-----KSAPTTPKEPAPTTPK----KPAPTTPKEPAPTTPKEPTPTT 264
                                                                                                                                                                                                                                                                                                                                          --DNKPAPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS
                                                                                                                                                                                                                                                                                                                                                                       TTPKEPAPTTT-----KSAPTTPKEP------APTTTKEPAPTTPKEPAPTT 217
                                                                                                                                                                                                                                                                                                                                                                                                    PGSGSSTTQGQDVTLAPATEPASGSAATWGQDVTSVPVTRPALGSTTPPAHDVT---SAP 122
                                                                                          SAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVT
                                                                                                                                                                                   TKEPSPTTPKEPAPTT--TKSAPTTTKEPAPTT----TKSAPTTPKEPSPTTTK----E
                                                                                                                                                                                                                                               PKE--PAPTTKEP-----APTTPKEPAPTAPK----KPAPTTPKEPAPTTPKEPAPTT 311
                                                          TPKETAP----TTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPT
                                                                                                                                                      APDXRP-XPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVT
                              SAPDXRPXPGSTAPXAHGVTS----APDXRPXPGSTAPXAHGVTSAPDXRPX----PGST
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128..1899
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linear
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-AAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGT-APTTLKEPAP
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23.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Amino acid 144 is Y = which is the codon for Thr or or ACG; and Asn = AAT or AAC."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note- "The amino acids spanning 128 to 1899 constitute a repeated region wherein the 20 amino acids, 17 of which are fixed. The number of repeats varies from 1 to 40."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Amino acid 134 is X1 = Xaa
Xaa Xaa which is the codon for Pro or
CCC, CCA, or CCG; and Ala = GCT, GCC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Amino acid 147 is X2 = Xaa which is the codon for Pro or Ala wherein Pro or CCG; and Ala = GCT, GCC, GCA, or GCG."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 424.5; DB 4
Pred. No. 1.2e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4;
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US-08-276-967-2
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Patent No. 5851817
GENERAL INFORMATION:
APPLICANT: Hardy, Daniel M.
                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,967
FILING DATE: Submitted Herewith
CLASSIFICATION: 530
            NAME: Kitchell, Barbara S. REGISTRATION NUMBER: 33,928 REFERENCE/DOCKET NUMBER: UTCLECOMMUNICATION INFORMATION: TELEPHONE: 713-787-1400
                                                                                     ATTORNEY/AGENT INFORMATION: NAME: Kitchell, Barbara
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hardy, Daniel M.
APPLICANT: Garbers, David L.
TITLE OF INVENTION: Species-Specific
TITLE OF INVENTION: Sperm
                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                              STREET: P. O. CITY: Houston STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                958
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ZIP: 77210-4433
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713-789-2679
                                                                                                                                                                                    Release #1.0, Version
                                               UTSD:418\KIT
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-276-967-2
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2476 amino acid
TYPE: amino acid
694 AHFERCACPVSCQ-SPTPNCEL
                                    867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           366 TIPTEKSTVPT--KKPTVFKEPTLPPE-GPTVPAE-RPTTPPEGPAVPPKG--PTVLTE- 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          313 PSETSVSTEKPVAPTE----KPTVPSETYTTPTEKPMVHMEKPIVHT--EKPTVPT-EKP 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           406 PKEPAPTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPEEP 465
                                                                                          KPKDRATNSKATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPT 866
                                                                                                                                                EKTTESKITATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETA 806
                                                                                                                                                                                                                                                             VPTEKPIVPTEKHTIPTEKLTVLTERTTTPTERTTIPTEKPTVPTEKPSVPT-EKPTVPT
                                                                                                                                                                                                                                                                                                                                               GTAPTTLKEPAPTTPKKPAPKELAPT-TTKGPTSTT---SDKPAPTTPKETAPTTPKEPA 636
                               SRIAEAMLQTTTRPNQTPNSKL 888
                                                                                                                                                                                            -----EEPTIPTEKLTVPT--ERTTTPTKRTTTPTIRTTTPTI------RTTTPT
                                                                                                                                                                                                                           PKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTT 746
                                                                                                                                                                                                                                                                                   PTTPKKPAPTTPETPPP----TTSEVSTPT-----TTKEPTTIHKSPDESTPELSAEPT 686
                                                                                                                             ERTT------PTIRTTTPTERTT---IPTKKTT-----VPTEKTIIPT----
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                                                                -TTPQP-SPTLVPTQPAAVVMPST----
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Pred. No. 3.2e-19;
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                                                             --SATTVTPRTTIASCP---PN 693
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Search completed: April 26, 2002, 16:17:34 Job time: 245 sec

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Title:
Perfect score:
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Listing first 45 summaries
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                        Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000
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J. Clin: Invest. 87, 77-82, 1991
A;Title: Human bronchus and intestine express the same mucin gene.
A;Reference number: A61257; MUID:91086481
A;Reference number: A61257
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 'T',1925-1948,'TTS',1952-1954 <JAN>
A;Experimental source: bronchus
R;Xu, G.; Huan, L.; Khatri, I.; Sajjan, U.S.; McCool, D.; Wang, D.; Jones, C.; For:
Biochem. Biophys. Res. Commun. 183, 821-828, 1992
A;Title: Human intestinal mucin-like protein (MLP) is homologous with rat MLP in tl
A;Reference number: PQ0328; MUID:92198477
A;Reference number: PQ0328; MUID:92198477
A;Residues: 2328-2468 <XUG>
A;Cross-references: GB:M86523
A;Cross-references: GB:M86523
A;Experimental source: small intestine
A;Residues: 2328-2342,'K',2344-2354 <XUG1>
C.Centics: PQ0328
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A;Map position: 11p15-5-11p15-5
A;Map position: 11p15-5-11p15-5
C;Superfamily: von Willebrand factor; von Willebrand factor type A repeat C;Superfamily: von Willebrand factor; tandem repeat C;Reywords: glycoprotein; intestine; tandem repeat homology <VWC>
F;2766-2834/Domain: von Willebrand factor type C repeat homology <VWC>
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YSYQGNCTYVLVEEISPSVD-----NFGVYID
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                                                                                                                                                                                                                                                                                                           SPDESTPELSAEPTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETT
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                                                       NNTVEIVKVECEPPPMPTCSNGLQPVRVEDPDGCCWHWECDCYCTGWGD-PHYVTFDGLY
                                                                                                                                         KPQKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRP
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                                                                                                                TPSKPSSTPSKPTPGTKPPECPDFDPPR-
                            --RPHVFMPEVTPDMDYLPRVPNQGIIIN
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S-layer protein - Clostridium thermocellum C;Species: Clostridium thermocellum C;Species: Clostridium thermocellum C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #;Accession: T18262 Pa;Fujino, T.; Beguin, P.; Aubert, J.P. R;Fujino, T.; Beguin, P.; Aubert, J.P. Bacteriol. 175, 1891-1899, 1993 Partitle: Organization of a Clostridium thermocellum A;Title: Organization of a Clostridium thermocellum
                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-1664 · A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1664 <FUJ>
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KPAPTTPKEPAPTTPKEPTPTTPKEPAPTTKEPAPT-TPKEPAPTAPKKPAPTTPKEPAP 301
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31.0%;
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Pred. No.
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#text_change 15-0ct-1999

C;Genetics: A;Gene: car

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Query Match
Best Local Similarity
Matches 355; Conserv

Conservative

15.0%; Score 853; DB 2; 32.3%; Pred. No. 5.3e-30; tive 46; Mismatches 475

Length 1489; Indels

Gaps

49;

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RESULT 3
T31108
Cyst germination specific acidic repeat protein precursor - Phytophthora infestans C;Species: Phytophthora infestans (potato late blight agent)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C;Accession: T31108
R;Goernhardt, B.
Submitted to the EMBL Data Library, April 1998
A;Reference number: Z20986
A;Accession: T31108
A;Status: preliminary; translated from GB/EMBL/DDBJ
                      A:Status: preliminary; translated A:Molecule type: DNA A:Residues: 1-1489 <GOE>
        A; Cross-references: EMBL: AF061185;
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TTLAPKVTTTKKTITTTEIMNKPEETAKPKDRAT--NSKATTPKP-QKPTKAPKKPT---
                                                     TAAPKMTKETATTTEKTTESKITATTTQVTSTTTQDTT------
                                                                                      TEETPYAPTEETTYEPTGETTYAPTEETTYAPTEETTYAPTEETTYAPTEETPYEPTEET
                                                                                                                  AEPTPKA-LENSPKEPG-----VPTTKTPAATKPEMTTTAKDKTTERDLRTTP----ETT
                                                                                                                                                 YAPAEETPYEPTEETTYAPTEETTYAPTEETMYAPIEETTYGPTEETTY-APTEATTYAP
                                                                                                                                                                            KETAPTTPKEPAPTTPKKPAPTTPETPPPTTSEVSTPTTTKEPT--TIHKSPDESTPELS
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                                                                                                                                                                                                          EETTYAPTEETTYAPAEETPYEPTEETTYAPTEETTYAPTEETTYAPTEETTYAPTEETT
                                                                                                                                                                                                                             -----TLKEPAPTTPKKP-----APKE---LAPT--TTKGPTSTTSDKPAPTTP
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                                                                                                                                                                                                                                                                                                                              EETTYAPTEETTYAPTEETTYAPTEETTYAPTEETTYAPAEETPYEPTEETTYAPTEETT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TKKKPTPKPPVVDEAGSGLDNGDFKYTTPDTSTT-----QHNKVSTSPKITTAKPINPR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTEATTYAPTEETPYAPTEETTYEPTGETTYAPTEETTYAPTEETTYAPTEETTYAPTEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTEETTYASTEETTYAPTEETTYAPAEETPYEPTEETTYAPTEETTYAPTEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TEETTYAPTEETPYEPTEETTYAPTKETTYAPT---EETTYASTEETTYAPTEETTYAPA
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                             -TEETTYEPTEETTYAPTEETTYAPTEETTYAPTEETMYAPIDETTYGPTEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -PNSDT----SKETSLTVNKETTVETKETTT---TNKQTSTD
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hypothetical protein F35A5.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
C;Accession: T16251
R;Leimbach, D.
R;Leimbach, D.
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A; Introns: 1272/2
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A;Experimental source: strain Bristol N2; clone F35A5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KNPTKKWKPPWEDETPVEEVKEPPVPEKKAPVLKKKDPAPAAKARDPSPSKAAPKKVEPS
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                                                                                                                                                                                                                                                                                                    APTAPKKPAP-----TTPKEPAPTTPKEPAPTTTKEP----SPTTPKEPAPTTTKSAPT 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPVKNPVKKWRPPWEDDETPADDVSKPTDAKKTPSLAKKDPAPAKESLKPKADTKAPAKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EAPAKKTPVLKRKEPAAKDTAKPATSKTPETPEKKDPVKPRDSSPKKVAAKPDSAQAPA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEPTPTTP----KEPASTTPKEP----TP-TTIKSAPTTPKEPAPTTTKSAPTTPKEPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PKKAAPAVKPRDSSPKKATPLQADPKAQEVPPTPVKNPVKKYKPPWEVDDEDPVEEVKQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ETQSIEKTSAKDLAPTSKVLAKPTPKAE----TTTKGPA----
{\tt T--EVPPAVVKKPEPVAKSRDPSPKKAK-AEPNSP--VVPPTPVKNPVKKWKPPWEDDDA}
                                                              TPKEPAPTTTKKPAPTA-PKEPAPTTPKETAPTTPKKLTPTTP----
                                                                                                                                PEKK-TPVLAKKAPTKPDSEAAADPVSGPSSKDPKLAKKAPVKPRDPSPMKAVPIKPAPK
                                                                                                                                                                                               TTKEPAPTTTKSAPTTP-KEPSPTTTKEPAPTTPK--EPAPTTPKKPAP--TTPKEPAPT 388
                                                                                                                                                                                                                                                                 APAAVKKPEPISKPKDTAPKKAEPNSPVVP-PTPVKNPVKKWKPPWEDDDAPAKPVSLPE
                                                                                                                                                                                                                                                                                                                                                                                                  RDPSPKKVAPTAPEKKTPVLAKKEPAGPADSKTKEPEKSKPRDPSPKKAVPAKPVPKTEV
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28.0%;
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Pred. No. 7.2e-28;
)2; Mismatches 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTTPEELAPTTPEEP-----TPTTPEEPAPTTPKAAAPNTPKEPAPTTPKEPAPTT-PKE
                                                                                                                                                                                                 TKPDSEAAADPVSGPTSKDPKLSKKAPVEKPKPTTDPKDDKLKPSPAKKPEKAPEPAAPK
                                                                                                                                                                                                                                                                   AAK-PDPKIPEV-PPTPVKNPVKKWKPPWEDDDEPSEPVSAPEPEKKTPVLAKKAPTKPA 1089
                                                                                                                                                                                                                                                                                      TPETPPPTTSEVSTPTTTKEPTTIHKSP----DESTPELSA-EP---TPKALENSPKEPG
                                                                                                                                                                                                                                                                                                                                                                                                      K-KEPEKPKD-APKVAAKPRDPSPKKAVPE--KEPAKVAAKPRDLSPKKAIPIPANTQEA 974
                                                                                                                                                                                                                                                                                                                                                                                                                                      KGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPT----TPKKPAP----KEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSPKKAEPNSPVVP----PTPVKNPVKKW-KPPWEDDDEPTEEVKKPSE--PEKKTPVLA
 ADFTMPAPKKPDTEDP
                                                                                                                                                               MTKETATTTEKTTESKITATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTE 797
                                                                                                                                                                                                                                                                                                                                   PPTPVKNPVKKWKPPWEDDDEPAEPVSAPEPEKKTPVLAKKAPAKPRDP---SPKKAAPV 1031
                                                                                                                                                                                                                                                                                                                                                                      APTTTKGPTS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPT-TTKEPTSTTSDKPAPTTP
                                 ---TTPTPRKMTSTMP
                                                                                                 IMNKPEETAKPKDRATNSKATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPK-----
                                                                                                                                 KWKPVWDDDPDEPEADFTVPAPSKKPDTEDPADPLG--
                                                                                                                                                                                                                                 PTTKTPAAT-----KPEMTTTAKDKTTERDLRTTPETT--TAAPK 737
                                                                                                                                                                                                                                                                                                                                                                      -TTSDKP----APTTPKET----
                                                                     PKPKEVSKEPPKPTEPPKP-AAPKKWKPPWEDDPDEPE 1243
                                                                                                                                                                                                                                                                                                                                                                        APTTPKEPAPTTPKKPAPT
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glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - yeast (Saccharomyces cerevisiae) N;Alternate names: extracellular glucoamylase; mucin-like protein MUC1; prot;Species: Saccharomyces cerevisiae C;Species: Saccharomyces cerevisiae C;Date: 10-sep-1999 #sequence_revision 10-sep-1999 #text_change 12-Nov-1999 C;Accession: S48478; A26877; B26877; S27281; JC6123 R;Yamashita, I.; Nakamura, M.; Fukui, S.
J. Bacteriol. 169, 2142-2149, 1987
A;Title: Gene fusion is a possible mechanism A;Reference number: A91831; MUID:87194600
A;Accession: A26877 submitted to the EMBL Data A; Reference number: S48478 A;Cross-references: EMBL:M16165; NID:g172523; PIDN:AAA35015.1; R;Pardo, J.M.; Ianez, E.; Zalacain, M.; Claros, M.G.; Jimenez, FEBS Lett. 239, 179-184, 1988 A; Residues: 1-1367 < ROW> A; Cross-references: GB:Z47047; A; Molecule type: R; Rowley, A; Title: Similar short elements in the 5' A; Reference number: S27281; MUID:89031230 A; Accession: S27281 A;Cross-references: EMBL:M16164; NID:g172522; A;Accession: B26877 A; Molecule type: DNA A; Residues: 1-242 <YAM> A; Accession: A; Molecule type: DNA A; Residues: 1-31 <PAR> A;Cross-references: EMBL:X R;Lambrechts, M.G.; Bauer, A; Molecule type: DNA A; Residues: 762-1331 S48478 DNA EMBL:X13857; NID:g4551; PIDN:CAA32069.1; PID:g4552 Bauer, F.F.; Marmur, J.; Pretorius, I.S. <YA2> Library, October EMBL: Z38061; Fukui, S. regions NID:g603997; underlying PIDN:AAA35014.1; of the the STA2 PID:g763364; protein MUC1; protein evolution and PID:g172526 PID:g172525 SGAof GSPDB:GN00009 genes STAL from Sacc

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A;Gene: SGD:MUC1; STA2; MAL5; DEX2; SGD:S00014;
A;Cross-references: MIPS:YIR019c; SGD:S0001458
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A: Title: Mucl. a mucin-like protein that is regula
A: Reference number: JC6123; MUID:96323237
A: Accession: JC6123
A: Status: nucleic acid sequence not shown
A: Molecule type: DNA
A: Residues: 1-1367 < LAM>
A: Cross-references: GB:U30626; NID:g1304386; PIDN:
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GSQTETSVSSTTETTIVPTKTTTSVTTPSTTTITTTVCSTGINSAGETTSGCSPKTVTTT
                           GVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITAT
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                                                                                                                 SAPVPTPSSSTTESSVAPVPTPSSSSNTTSSAPSSTPFSSSTESSSVPVPTPSSSTTESS
                                                                                     PAPTTPETPPPTTSEVSTPT-----TTKEPTTIHKSPDESTPELSAEPTPKALENSPKEP
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                                                                                                                                                                            SSSAPVPTPS-SSTTESSSAPVTSSTTESSSAPVPTPSSSTTESSSAPVPTPSSSTTESS
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R;Rubinstein, A.L.; Broadwater, A.H.; Lowrey, K.; Bedinger, P.A. submitted to the EMBL Data Library, June 1994
A;Description: Pex genes: pollen-specific genes with extensin-like A;Reference number: $49915
A;Accession: $49915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA A;Residues: 1-1188 <RUB>
A;Residues: 1-1188 <RUB>
A;Cross-references: EMBL:234465; NID:g600117; PIDN:CAA84230.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 extensin-like protein - maize
C:Species: Zea mays (maize)
C:Date: 05-Mar-1995 #sequence_revision 12-May-1995 #text_change 29-Oct-1999
C:Accession: $49915
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TTPKETAP----TTP----KKLTPTTPEKLAPTTPEKPAP-----TTPEELAPTTPEEPT
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                                                                                                                                 EPSPTTTKEPAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTTTKKPAPTAPKEPAP
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Pred. No. 4e-27;
Mismatches 359; Indels 122;
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R; yotov, W.V.; St-Arnaud, R.
Genes Dev. 10, 1763-1772, 1996
A; Title: Differential splicing-in of a proline-rich exon
A; Reference number: 200889; MUID:96312450
A; Accession: T30826
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nascent polypeptide-associated complex alpha Ny Alternate names: alpha-NAC protein . C:Species: Mus musculus (house mouse) C:Date: 22-Oct-1999 #sequence_revision 22-Oct C:Accession: T30826
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A; Residues: 1-2187 <YOT>
A; Residues: 1-2187 <YOT>
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A;Introns: 24/1: 1996/1; 2024/3; 2050/3; 2099/3; 2142/3; 2183/3
A;Introns: 24/1: 1996/1; 2024/3; 2050/3; 2099/3; 2142/3; 2183/3
A;Note: differential splicing converts alphaNAC into a tissue-specific C;Keywords: alternative splicing; DNA binding; transcription factor
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A;Gene: Naca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAPKSSPPHVVVSSPPPVVKSSPPPAPVSSPPLTPKPASPPAHVSSPPEVVKPSTP--PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -KEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LKE---PA----PTTPKK---PAPKELAPTTTKE---PTSTTSDKPAPTTPKGTAPTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTTPEEPAPTTPKAAAPNTPKE-PAPTTPKEPAPTTPKETAPTTPKGTAPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAEPTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KSPPPPAPISSPPPPVKSPPPPAPVS--SPPPPPVKSPPPPAPVSSPPPPIKSPPPPAPVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MSSPPPPPEVKSPPPPAPVSSPPPPVKSPPPPAPVSSPP---PPVKSPPPPAPVSSPPPPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VKSSPPPAPVSSPPATPKSSPPPAPVNLPPPEVKSSPPPTPVSSPPPA---PKSSPPPAP
                                                                                                                                                                                                                                                                               VETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPA
                                                                                                                                                                                                                                                                                                                                                     VTTPDTSTTQHNKVSTSPKITTAKPINPRPSLPPNSDTSKE---
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                                                                                                                                                                                                                                              APSNEATIVPTEIPTSLKNALAAATPKETLATSIPKVTSPS----PQKTPKSVSLKGAPA
                                  APKTAVSKEIPSKGVTAVPLEISLPLKETSKSATPGEKSASSPKRSPKTAGPKE---TPP
 KEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTT--PKEPAP----TTPKEPAPTT
                                                                                                        LAETPTYPKKSPKPAASKKTPATPSPEGVTAVPLEIPPCSKKAPKTAAPKESSATSSSKR
                                                                                                                                         IKSAPTTPKE-PAPTTTKSAPTTPK---
                                                                                                                                                                            MTSKKATEIAASKDVSPSQFPKEVPLLQHVPPTSPPKSPVSDTLSGALTSPPPKGP-PAT
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27.7%;
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Pred. No. 1.6e-26;
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                                                                     TPKEPAPTTPKK-PAPTTPKEPAPTTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKTPKTAVPKETSAPSEGVTAVPLEIPPSPRKAPKTAAPKETPAPS--PEGATTAPVQIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QKAPKTAVPKQIPTPEDAVTILAGSPLSPKKASKTAAPKEAPATPSVGVIAVSGEISPSP 1209
                                                                                      APKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPNQTPNSK 887
                                                                                                                     QTAPKEATTIPSCKKAAATETPIETSTAPSLEGAPKETSE----TSVSKVLMSSP-----
                                                                                                                                                                                   T--SLAQTAPPSLQKAPSTTIPKENLAAPAV----LPVSSKSPAAPARASASLSPATAAP 1665
                                                                                                                                                                                                               TKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTSTTTQ
                                                                                                                                                                                                                                               KNPSSHKKTSKTIELKEAPATLPPSPTKSPKIPSSKKAPRT--SAPKEFPASPSIK-PVT
                                                                                                                                                                                                                                                                         TSEVSTPITTK-----EPTTIHKSPDESTPELSAEPTPKALENSPKE-PGVPTTKTPAA 707
                                                                                                                                                                                                                                                                                                                                                                      VGPKETSLEGATAVPLEIPPSHKKAPKTVDPKQVPLTPSPK-DAPTTLAE-SPSSPKK-A
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 DSHISPVS-DACSTGTTTP
                             LVEVNPKSEDAGGAEGETP
                                                                                                                                                  DTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQKPTK
                                                                                                                                                                                                                                                                                                          PKTAAPPSER-VTTVPPEKPA-TPQKASGTTASKVPVPAETQEVAVSSRETPVTPAVPPV 1554
                                                                                                                                                                                                                                                                                                                              PKELAPTTTKGPTSTISDKPAPTTPKETAPTTPKEPAPTTPKKPAPTTPETP-----PT
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                                                                  PTATSSGK 1752
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ESULT 8

R;Ligtenberg, M.J.L.; Vos, H.L.; Gennissen, J. Biol. Chem. 265, 5573-5578, 1990
A;Title: Episialin, a carcinoma-associated A;Reference number: A35175; MUID:90202794 mucin 1 precursor, repetitive splice form A [validated] - human N;Alternate names: breast carcinoma-associated DF3 antigen; core ncreatic mucin; polymorphic epithelial mucin (PEM)
N;Contains: mucin 1 precursor, epithelial tumor antigen splice 1 A;Accession: B35175 A;Molecule type: mRNA A;Residues: 1-19,29-952,1033-1344 A;Cross-references: GB:M32738; GB:J05288; NID:g182121; PIDN:AAA35804.1; A; Accession: A35175 A; Experimental source: splice form A A; Note: GenBank entries HUMEPISIAl ar A; Residues: 1-952, 1033-1344 A; Molecule type: mRNA ;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Jun-2000;Accession: A35175; B35175; A35886; A35887; S10572; S40293; A36735; PX0066; Ligtenberg, M.J.L.; Vos, H.L.; Gennissen, A.M.C.; Hilkens, J. ;Species: Homo sapiens (man) <LIG1> and HUMEPISIA2 mucin, antigen splice form; İs present generated only core уd the protein KP39; D amino-and polymorphic mucin PID:g182124; carboxyl episia gene

the amino-and hig, T.; Peat,

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A; Scacus: incr Compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 1-19,29-1109,'S',1111-1339,'A',1341-1344 <LAN>
A; Cross-references: GB:JO5582; NID:g198598; PIDN:AAA60019.1; PID:g189599
A; Note: GenBank entry HUMPANMU contains four fewer copies of the tandemly repeated seque
R; Wreschner, D.H.; Hareuveni, M.; Tsarfaty, I.; Smorodinsky, N.; Horev, J.; Zaretsky, J.
Eur. J. Blochem. 189, 463-473, 1990
A; Title: Human epithelial tumor antigen cDNA sequences. Differential splicing may genera
A; Reference number: $10571
A; Molecule type: mRNA
A; Residues: 1-19,29-155,'p',157-175,'p',177-182,'A',184-212,1033-1344 <WRE>
A; Cross-references: EMBL:X52229; NID:g37053
R; Wreschner, D.H.
submitted to the EMBL Data Library, March 1990
A; Reference number: $40293
A; Accession: $40293
A; Commun. 165, 644-649, 1989
A; Title: Sequence analysis of the 5' region of the human DF3 breast carcinoma-associated
A; Reference number: $40735; MUID:90088473
A; Molecule type: mRNA
A; Residues: 1-19,29-155, 'p',157-175, 'p',177-182, 'A',184-212,1033-1037, 'A',1039-1344 <WR2
A; Accession: A36735; MUID:90088473
A; Molecule type: mRNA
A; Residues: 1-19,29-155, 'p',157-175, 'p',177-182, 'A',184-212,1033-1037, 'A',1039-1344 <WR2
A; Accession: A36735; MUID:90088473
A; Molecule type: mRNA
A; Residues: 1-19,29-155, 'p',157-175, 'p',177-182, 'A',184-212,1033-1037, 'A',1039-1344 <WR2
A; Accession: A36735; MUID:90088473
                                                                                                                                 A;Gene: GDB:MUC1; PUM
A;Cross-references: GDB:120705; OMIM:15
A;Map position: 1q21-1q23
A;Introns: 20/1; 62/3; 1165/3; 1184/2;
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                                                                                                                                                                                                                                                                                                 A:NOTE: undetermined tyrosine residues in the carboxyl-terminal non-repetitive region C:Comment: This protein is length polymorphic. Individuals may have between 21 and 1: partial repeats. The repeat shown is defined by Smal nuclease sites.
C:Comment: Serine and threonine residues in the tandem repeat domain are extensively C:Comment: For an alternative splice form without a tandem repeat domain, see PIR:S48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 998-1011, 'ES', 1014-1017;1018-1032, 'T', 1034-1037;1038-1057
A; Experimental source: gastric carcinoma cell
A; Zrihan-Licht, S.; Baruch, A.; Elroy-Stein, O.; Keydar, I.; Wreschnei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R.Masuzawa, Y.; Miyauchi, T.; Hamanoue; M.; Ando, S.;
J. Biochem. 112, 609-615, 1992
A:Title: A novel core protein as well as polymorphic
A:Reference number: JX0235; MUID:93123189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: Tyrosine phosphorylation of the MUC1 A; Reference number: S51026; MUID:95080414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Contents: annotation
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A; Residues: 1-19, 29-992, 1033-1344 <GEN>
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                  Superfamily: polymorphic epithelial mucin glycoprotein; phosphoprotein; Keywords: alternative splicing; duplication; glycoprotein; phosphoprotein; 1-1344/Product: mucin 1 precursor, splice form A #status predicted <PREA>
   ·62/Region:
       mucin 1
amino-terminal
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non-repetitive
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J.; Takao, ;
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GB:J05288; NID:g182126; PIDN:AAA35806.1; PID:g182129; GB
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F;1-19,29-32/Domain: signal sequence #link PREB #status predicted <SIGB>
F;1-19,29-1344/Product: mucin 1 precursor, splice form B #status predicted <P
F;1-19,29-212,1033-1344/Product: mucin 1 precursor, epithelial tumor antigen F;138-1017/Region: 20-residue repeats (GSTAPPAHGVTSAPDTRPAP)
F;1143-1344/Region: mucin 1 carboxyl-terminal non-repetitive F;1243-1372/Domain: transmembrane #status predicted <TRM>
F;1245-1272/Domain: site: phosphate (Tyr) (covalent) #status predicted
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                                                                          ESTPELSAEPTPKALENSPKEPGVPTTKTPAA-
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Pred. No. 3.le-22;
B; Mismatches 472
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                                                                                                          -TAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPD
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	449	
APTTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKE 360	Qy 307 PAPTTTKEPSPT	
PAPTTPKEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAPTTPKE 306	Qy 251 EPAPTTPKEPTPTT- Db 397 -TAGAVPKASTGTTP	
	Db 338 KPAPPPPPQQLPKAA	
	Qy 204 EPAPTTPKEPAPTTT	
AEAKPVPATASLMATKVTAEAKPAPSPSVPKATTDTKAVTATAPKAGPDVKPAVAVCAEA 337	Db 278 AEAKPVPATASLMAT	
APTT 203	Qy 178 TPKEPAPTT	
TSPTIPCSSAEAKPLTAASPTASKAT	0	
A SANDE I VE ANTALALATA VERREDE - TORREDE STUDVEN A RUTTER TPTT I KSAPT	173 ADTEVI	
LPPNSDTSKETSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKDL 122	65 LPPNSDT	
	113	
PVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRPS 64	;	
11.8%; Score 671; DB 2; Length 1151; nilarity 25.9%; Pred. No. 3e-22; Conservative 100; Mismatches 419; Indels 292; Gaps 55;		
inary; translated from GB/EMBL/DDBJ MRNA 151 <shi> 152 : EMBL:D88440; NID:d1177138; PID:d1025045; PIDN:BAA24137.1</shi>	A;Status: preliminary; tro A;Molecule type: mRNA A;Residues: 1-1151 <shi> A;Cross-references: EMBL:</shi>	
Cell Sci. 110, 301-3047, 1997 Title: A nuclear matrix-associated high molecular mass nuclear antigen, HMNA, of chick Reference number: Z18955; MUID:9803440 Accession: T18335	J. Cell Sci. 110, 3031-3041. A;Title: A nuclear matrix-ass A;Reference number: Z18955; M A;Accession: T18535	
es: Gallus gallus (CHICKEH) 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 sion: T18535 da K : Harata M : Mizuno, S	C;Species: Gallus gallus (C;Date: 15-Oct-1999 #seque C;Accession: T18535	
mass nuclear antigen - chicken (fragment)	RESULT 9 T18535 high molecular mass nuclea	
ASGSASGSASTLVHNGTSARATTTPASKSTPFSIPS 1085	Db 1050 ASGSASGSASTLVHNG	
ICNGKPVDGLTTLRNGTLVAFRGHYFWMLSPFSPPS 981	QY 946 ICNGKPVDGLTTLRNG	_
SKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLSDETN 945 : : : : : : :	Oy 886 SKLVEVNPKSEDAGGA : : : Db 1004 AHGVTSAPDTRPAPGS	
TKKEKIMPRVRKEKITETERKMISIMPELNETSRIAEAMLQT-TIKENUTEN 865 : :: : : :	Qy 834 STKKEKIMPRVRKEKT	
TAPPAHG	Db 889 SAPDTRPAPGSTAPPA	
-EIMKPEETAKPKDRATNSKATTPKPQKPTKAPKKPT	Qy 776 TLKTTTLAPKVTTTKKTITTT-	_
TRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVT 888	Db 833 TRPAPGSTAPPAHGVT	_

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              628 LPSSPVASAMHAKVTPRPLPASPVPMAASPASLGPDAARVALATNAASPGAKPEAAGGNG 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           451 -PTTP------EEPTPTTP----EEPAPTTP------KAAAPNTPKE-----
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                            890 EVNPKSEDAGGAEGE 904
                                                                                    830 KKPTSTKKPKIMPRVRKPKTIPTPRKMISIMPELNPISRIAEAMLQIITRPNQTPNSKLV 889
                                                                                                                                                 770 TPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQKPTKAP 829
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                                                                                                                                                                                                                                                                                                                                                                                                                         GGATQMSPMGAANTQMSPMGATTTQMSPMGAAATTQPSPMGAAATQVTATSAGNTMQVSP 807
                                                                                                                                                                                IGVTEASPSADGARLSPGPTAATDGPKASPAATADVTEAATD--VTAAATAVPA----EA 1029
                                                                                                                                                                                                           EMTTTAKDKTTERDLRTTPETTTAAPKMT-KETATTTEKTTESKITATTTQVTSTTTQDT 769
                                                                                                                                                                                                                                         PPPPTIPPSTAQTSPQPMSKSPPPDPPKAPSAAAQTSPAAHVANASPGV-TAVSPA---P
                                                                                                                                                                                                                                                                    PTTSEVSTPTTTKEPTTIHKSPDESTPEL--SAEPTPKALENSPKEPGVPTTKTPAATKP 710
                                                                                                                                                                                                                                                                                                                                   ----TSTTSDKP-APTTPKET---APTTPKEP---APTTPKKP-APTTPETPP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---TLKEPAPTTPKKPAPKELAPTTTKEP----TSTTSDKPAPTTP 555
                                                         PAVGDGQQQMTPGAAQSVPP-
                                                              -VTEAAVQ----
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hypothetical protein F16F9.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:pate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T25697
R;Fulton, B.
submitted to the EMBL Data Library, August 1996
A;Description: The sequence of C. elegans cosmid F16F9.
A;Reference number: Z20071
A;Accession: T25697
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Access: 1-1229 <FUL>
A;Cross-references: EMBL:U67956; PIDN:AAB07691.1; GSPDB:GN00028; CESP:F16F9.2
A;Experimental source: strain Bristol N2; clone F16F9
                                                                                                                                                                                   A; Map position: X
A; Introns: 35/1; 361/1; 384/1; 482/2; 517/1; 971/1; 1021/2; 1179/3
                                                                                                                                                                                                                                      A; Gene: CESP:F16F9.2
                                                   Query Match
Best Local Similarity
Matches 307; Conserv
33 KVTT-PDTSTTQ----HNKVSTSPKITTA-KPINPRPSLPPNSDT-----SKETSLTVN 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10
                                                        Conservative
                                                                                 11.6%;
                                                           78;
                                                        Score 659.5; DB 2;
Pred. No. 1e-21;
8; Mismatches 339;
                                                                                                            Length 1229;
                                                              Indels
                                                                 333;
                                                              Gaps
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119 KVTTSTDASTTNAPTTGKDSTTPEIITGTVVINSKSESVTDMSTTRFSTTLSPTTELLTS 178

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HTTTDAAFVTATEASLNDGSDKKIIDEAQPTDEIRRA 1059
                           KTTPTPRKMTSTMPELN------PTSRIAEA
                                                                                                                              SKITATTTQ-VTST---TTQDTTPFKITTLKTTTLAPKVT
                                                                                                                                                        TTTSESAAF ITGESPENTALQSSSQKSEENESSAEKPGARRDFVPKKHKTTVKPAETTSA
                                                                                                                                                                                                                                      HKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPE
                                                                                                                                                                                                                                                                                         TTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPTTPE--TPPPTTSE-VSTPTTTKEPTTI
                                                   ----INNTQISQPKPTDISKTDALSSLISGLIGSFTKAPMAPTI
                                                                               TAKPKDRATNSKATTPKPQ-----
                                                                                                      VAASTTTTEPITTTEKSTTLETTPIEATTLNEVTGPAFVTGAPVDETTINTLELLSK---
                                                                                                                                                                                                                                                                 TEKEKVVQTTPITTEKSTTQEETTTTTTTTEKTTSKTTTEKPTTSESATTETTTSEPST-
                                                                                                                                                                                                                                                                                                                       STPRQLPERWKATVNKFKHNLEVLKEKKRLLKEKESTSTTGSDSSETTTVVAENIDEVTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E------PKETAP 419
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                                                                                                                                                                                    -----APKMTKETATTTEKTTE
                                                                                                                                                                                                              -----TVDTSSATTEESSTAAETTTTSAE---TSE
                                                                                                                                                                                                                                                                                                                                                  KKPAPKELAPTTTKGP-----TS
                                                                            ----KPTKAPKKPTSTKKPKTMPRVRKP
                            872
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extensin class 1

precursor -

C;Species: Homo sapiens (man) C;Date: 29-May-1998 #sequence C;Accession: I38346

#sequence_revision

29-May-1998 #text_change

21-Jul-2000

elastic titin -

human (fragment)

I38346

11

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C; Species: viy...
C; Date: 16-701-1999 #sequence_rev...
C; Date: 16-701-1999 #sequence_rev...
C; Accession: T11622; S54155
R; Arsenijevic-Maksimovic, I.; Broughton, W.J.; Krause, A. Mol. Plant Microbe Interact. 10, 95-101, 1997
A; Title: Rhizobia modulate root-hair-specific expression
- Terrance number: 217301; MUID: 97155574
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A.Gene: Ext26G
A:Gene: Ext26G
C:Superfamily: hydroxyproline-rich glycoprotein
C:Keywords: glycoprotein; hydroxyproline
F:1-23/Domain: signal sequence #status predicted <SIG>F:24-489/Product: extensin class 1 #status predicted <MANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Experimental source: sub_species Red caloona R; Arsenijevic-Maksimovic, I.; Broughton, W.J.; Krause, submitted to the EMBL Data Library, April 1995 A; Description: A class of root-hair specific extensins A; Reference number: $54155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qy
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A; Residues: 326-489 <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: A; Accession: S54155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-489 < ARS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type:
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Best Local
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Spate: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change
Accession: T11622; S54155
         423
                               596 KKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPTTPETPPP 653
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                                                                                                                                                                                NTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAPKELA
         SPP----
                                                                        ----KSPPPPSPSPPPPYYYKSPPPPSPSPSPPPPYYYKSPPPPSPSPSPPPYYYKSPPPPSP
                                                                                                                                             PSPSPPPPYYYKSPPPPSPSPPPPYYYYKSPPPPPSPSPPPPYVYXSPPPPSPSPPPPYYY-
                                                                                                                                                                                                                     PPPPYYYKSPPPGSPSPPPPYYYKSPPPGSPSPPPPYYYKSPPPPSSSPPPPPYYYKSPPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                               PSPSPPPPYYYKSPPPPSPSPPPPYYYKSPPPPS--PSPPPPYYYKSPPPPSPSPPPPYY 141
                                                                                                                                                                                                                                                                                              YKSPPPPSPSPPPYYYKSPPPPSPSPSPPPPYYYKSPP-------PPSPSPSPPPP
                                                                                                                                                                                                                                                                                                                                                                                                          PKEPAPTTPKEPAPTTKEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPKEPSP 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTPKKPAPTTPKEPAPTTPKEPTPTTPKEPAPTTKEPAPTTP---KEPAPTAPKKPAPTT 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PKQTPPYYYNAPPYYYKSPPP-----PSPSPP------PPPYYHKYPPYYYKSPPP 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149;
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-PPYVYKSPPPPSPSPPPPYYYKSPPPPSPSPPPPYYYKSPPPPSPSPPPP
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3; Mismatches
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Pred. No. 5.7e-21
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R;Labeit, S.; Kolmerer, B.
Science 270, 293-296, 1995
A;Hitle: Titins: giant proteins in charge of muscle ultrastructure and elasticity.
A;Acference number: A57430; MUID:96026330
A;Accession: I38346
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-7962 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X90569;
C;Genetics:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VPEVPKKPVPEEKIPVPVAKKKEAPPAKVPEVQKGVVTEEKITIVTQREESP----PPAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - PKITTAKPINPRPSLPPNSDTSKETSLT---VNKETTVETKETTTTNKQTSTDGKEKTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    EEEAEVTEYEVMEEPEEYVVEEKLHIISKRVEAEPAEVTERQEKKIVLKPKIPAKIEEPP
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                                                                                                                                               KPAPTAPKEPAPTTPKETAPTTPKKLTPTTPEK-----LAPTTPEKPAPTTPEELAPT
                                                                                                                                                                                                                                                                                                                    TEKHMQITQEEKVLVAVTKKEAPPKARVPEEPKRAVPEEKVLKLKPKREEEPPAKVTEFR 6361
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                                                 VPMKPKRVVAEEKVPVPRKEVAPPVRVPEVPKELEPEEVAFEEEVVTHVEEYLVEEEEEEY
                                                                                                                   KAVP-EEKVPVP-IPKKLKPPPPK--VPEEPKKVFEEKIHISITKREKEQVTEP---AAK
                                                                                                                                                                                  EEYEPTEEYDQYEEYEEREYERYEEHEEYITEPEKPIPVKPVPEEPVPTKPKAPPAKVLK
                                                                                                                                                                                                                                                   KRYVKEEKVSIEAPKREPQPIKEVTIMEEKERAYTLEEEAVSVQREEEYEEYEEYDYKEF
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                                                                                  TPEEPTPTTPEEPAPTTPKAAAP--NTPKEPAPTTPKEPA-
PTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTS 544
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A; Residues: 1-761 <STO>
A; Cross-references: GB: AE002093;
                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Sequence and analysis of chromosome A;Reference number: A84420; MUID:20083487 A;Accession: C84672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   euss, D.; Nierman, W.C.; Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
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A;Map position: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQKPT 826
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                                                                                                                                                                          PTPKAETTTKGPALTTP---KEPTPT-TPKEPASTTPKEPTPTTIKSAPTTPKEPAPTTI 187
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PPIKPPVHKPPTPIYSPPIKPPPVHKPPTPIYSPPIKPPPVHKPPTPTYSPPVKPPPVHK 241
                                                                                        KSAPTTEKEPAPTTTKEPAP---TTPKEPAPTTTKSAPTTP----KEPAPT---
                                                                                                                                        PPPIQKPPTYSPPIYPPPIQKPPTPTYSPPIYPPPIQKPPTPTYSPPIYPPPIQKPPTPT 128
                                                                                                                                                                                                                   Conservative
                                                                     ---PPIQKPPTPSYSPPVKPPPV---QMPPTPTYSPPIKPPPVHKPPTPTYS
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                                                                                                                                                                                                                                    11.1%;
31.1%;
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; Pred. No. 9.7e-21;
44; Mismatches 354;
                                                                                                                                                                                                                                                                                                                                                            NID:g5306260; PIDN:AAD41992
                                 -KEPTP--TTPKEPAPTTKEPAPT-TPKEPAPTAPK 289
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A:Molecule type: DNA
A:Residues: 1-3507 <FAV>
A:Cross-references: EMBL:U13646; PIDN:AAC24418.1; GSPDB:GN00021; CESP:ZK783.1
A:Experimental source: strain Bristol N2; Clone ZK783
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14

134513
hypothetical protein ZK783.1 - Caemorhabditis elegans
C:Species: Caemorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change
C:Accession: T34513
R:Favello, A.; Vaudin, M.
submitted to the EMBL Data Library, August 1994
A:Description: The sequence of C. elegans cosmid ZK783.
A:Reference number: Z21536
A:Accession: T34513
                                                                                                                                                                                                                                                                             A; Introns: 14/1; 48/2; 3504/1
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A;Map position: 3
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Best Local Similarity
Matches 252; Conserv
                                            2002
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                                 DMTSSKS-PENVTMSSESPEVSTSSSKSTTASETTVSSTPSESSSSEAPLTSSPATTTEV
                                                                                                                                      KKKPTPKPPVVDEAGSGLDN-GDFKVTT----PDTSTTQHNKVSTSPKITTA-----K 57
IEKTSAKDLAP----TSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTP
                                                                 PINPRPSLPPN---SDTSKETSLTVNKETTV-ETKETTTTNKQTSTDGKEKTTSAKETQS
                                                                                                       KKQPNREKIEIDEENSSSSNSGQEKPTTKGIVSSTSATSSESTTAEPHVTTSISSTTSTK
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                                                                                                                                                                            11.0%; Score 629; DB 2; 1
11arity 24.1%; Pred. No. 5.7e-20;
Conservative 158; Mismatches 416;
                                                                                                                                                                                                                                                                                         84/1; 196/3; 303/1;
                                                                                                                                                                                                                                                                                       381/1; 586/1;
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                                                                                                                                                                              Indels 218;
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                                                                                                                  VVTASSIPSEEPILSSVTSSSTPRVRLITGTPDDLIVSVTVPSHGNRRQNITASSV---P
                                                         SNSTSPIILPSES-LTTPQPPPTTTTTAKPATTSGKRGPPSIQPPAEMFTTPAP-----
                                                                                     EETAKPKDRATNSKATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPK----TTPTPRKMTST
                                                                                                                                                                               KLSSLFPESITSEAVTVSSR----APAEITMSSESHREISTVSSEPSEPEIPLSTTVSPN
                                                                                                                                                                                                          K-----PEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTT----
                                                                                                                                                                                                                                           SGSLESSTMSSTS-----SEPETNAPAVTVSSEASSTTLEENSSTSSP----TSSEASV
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nucleolar phosphoprotein - African clawed frog C;Species: Xenopus laevis (African clawed frog) C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change C;Accession: I51618; S57757 R;Cairns, C; McStay, B. J. Cell Sci. 108, 3339-3347, 1995 A;Title: Identification and cDNA cloning of a Xenopus nucleolar

24-Sep-1999

cloning of a Xenopus nucleolar phosphoprotein, xNopp

RESULT 151618

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A;Reference number: I51618; MUID:96019267
A;Accession: I51618
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-990 <CAI>A;Cross-references: EMBL:X88927; NID:g895920; PIDN:CAA61368.1; PID:g895921
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: xNopp180
C;Superfamily: nucleolus-cytoplasm shuttle phosphoprotein
C;Keywords: phosphoprotein
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754 ITATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTK--KTITTTEIMNKPEETA-KPKD 810
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                                                                                                                                                                                                                                                                            KPAPKELAPTTIKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTT--PKEPAPTTPKGTAPT 585
                                                                                                                                                                                                                                                                                                                  AAKSTPGKQVPTKKESSSSDSSSEDEKKSSAKPAVKTTPGKATS-----KPVVAS 611
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                                    SSE---DSSSDEDVSKAKKTNTAVSKSPV----TTPKAVPAAKKESSSESSDSEDEKQGG 835
                                                                  PKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESK 753
                                                                                                        ATAPPKKNPVAVNKDKPSSSSSSSSSGDDEKQKPKQAAAAKDVKQGAKAAKPTPKKAASS
                                                                                                                                        APTTPKK-PAPTTPETPPPTTSEVSTPTTTKE-PTTIHKSPDESTPELSAEPTPKALENS 693
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Db	Qy	Db	Qy	Db.
929 -RMAD 932	867 SRIAE 871	-	811 RATUSKATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPKTTPTP-RKMTSTMPELNPT 866	836 KNTSTTKIANSTPKAAAAECSEESSSEDEGKANGTSGKRKR 877
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Search completed: April 26, 2002, 16:19:22 Job time: 352 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

April 26, 2002, 16:19:35; Search time 47.4 Seconds (without alignments) 823.025 Million cell updates/sec

Title: Perfect score: Sequence: US-09-556-246-1_COPY_200_1263 5698

1 VKDNKKNRTKKKPTPKPPVV......VAALSTAKYKNWPESVYFFK 1064

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

100059 segs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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-!- SUBCELLULAR LOCATION: SECRETED!- TISSUE SPECIFICITY: COLON, KMALL INTESTINE, COLONIC TUMORS, BRONCHUS, CERVIX AND GALL BLADDER!- PTM: ALL CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN OR INTERCHAIN DISULFIDE BONDS (BY SIMILARITY)!- POLYMORPHISM: THE NUMBER OF REPEATS IS HIGHLY POLYMORPHIC AND VARIES AMONG DIFFERENT ALLELES!- SIMILARITY: THE N-TERMINAL DOMAIN SHOWS SOME SIMILARITY TO THAT OF SILKWORM HEMOCYTIN!- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).	i-	SEQUENCE FROM N.A. TISSUE-Intestine; MEDLINE-9413002; PubMed-8300571; Gum J.R. Jr., Hicks J.W., Toribara N.W., Siddiki B., Kim Y.S.; "Molecular cloning of human intestinal mucin (MUC2) cDNA. Identification of the amino terminus and overall sequence similarity to prepro-von Willebrand factor."; J. Biol. Chem. 269:2440-2446(1994). [2] SEQUENCE OF 626-1895 AND 4196-5179 FROM N.A. TISSUE-Colon; MEDLINE-93016075; PubMed=1400449; Gum J.R. Jr., Hicks J.W., Toribara N.W., Rothe EM., Lagace R.E., Kim Y.S.; "The human MUC2 intestinal mucin has cysteine-rich subdomains located J. Biol. Chem. 267:21375-21383(1992). [3]	LIT 1 LHUMAN STANDARD; PRT; 5179 AA. MUC2_HUMAN STANDARD; PRT; 5179 AA. Q22817; Q14878; 01-WN-1994 (Rel. 29, Created) 01-WN-1997 (Rel. 35, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) MUC1N 2 PRECERSOR (INTESTINAL MUCIN 2). HOMO sapiens (Human). EUKARIYOLA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1; MCBI_TaxID=9606;

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                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                       MEDLINE-320931; PubMed-8458832; Fujino T., Beguin P., Aubert J.-P.; Pujino T., Beguin P., Aubert J.-P.; "Organization of a Clostridium thermocellum gene cluster encoding the cellulosomal scaffolding protein CipA and a protein possibly involved in attachment of the cellulosome to the cell surface."; In Subsciptiol. 175:1891-1899(1993).

1. Subsciptiol. 175:1891-1899(1993).

1. Subsciptiol. RSSEMBLED INTO MONO-LAYERED CRYSTALLINE ARRAYS.

1. SUBCELLULAR LOCATION: CELL WALL.

1. SIMILARITY: CONTAINS 4 S-LAYER HOMOLOGY (SLH) DOMAINS.
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Q1-JUN-1994
Q1-JUN-1994
Q1-FEB-1996
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                             EMBL; X67506; CAA47841.1;
InterPro; IPR001119; SLH.
Pfam; PF00395; SLH; 3.
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UN-1994 (Rel. 29, Last sequence update)
UN-1996 (Rel. 33, Last annotation update)
SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER
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SLH_DOMAIN;
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Pred. No. 4.7e.
04; Mismatches
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T-P-S-D-E-P-
GLY/PRO/SER/THR-RICH.
SLH 1 (INCOMPLETE).
SLH 2.
SLH 3.
SLH 3 (INCOMPLETE).
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POTENTIAL.

CELL SURFACE GLYCOPROTEIN

4 X 156 AA APPROXIMATE REP
                                                                                     --TTTPTPTPSTT
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No. 4.7e-32;
TEIEEPTPSDVPGAIGGEHRA
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AMYH-YEAST

AMYH-YEAST

C P08640; P08868;

T 01-AUG-1988 (Rel. 08, Created)

T 01-EB-1995 (Rel. 31, Last sequence update)

T 01-EB-1995 (Rel. 31, Last annotation update)

T 01-EB-1995 (Rel. 40, Last annotation update)

T 20-AUG-2001 (Rel. 41, Last annotation update)

DE GLUCOAMYLASE S1/S2 PRECURSOR (EC 3:2.1.3) (GLUCAN 1,4-ALF

DE GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).

GN STA1 OR STA2 OR MAL5 OR YIR019C.

S accharomyces cerevisiae (Baker's yeast).

OS Saccharomyces cerevisiae (Baker's yeast).

OS Saccharomyces Saccharomycetaceae; Saccharomyces.
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STRAIN-S288C / AB972;

Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,

Barrell B.G., Connor R.; Copsey T., Dear S., Devlin K., Fraser

Churcher C.M., Connor R.; Copsey T., Dear S., Devlin K., Fraser

Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones

Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,

Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,

Walsh S.V., Whitehead S.;

Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-242 AND 762-1331 FROM MEDLINE-87194600; PubMed-3106330; Yamashita I., Nakamura M., Fukui S.; "Gene fusion is a possible mechanism"
                                          the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                 Yamashita I.,
"Gene fusion :
STA1.":
                                                                                                                                          This
                                                                                                                                                                                                                                                       FEBS
                                                                                                                                                                                                                                                                                    MEDLINE-89031230; PubMed-3141213; Pardo J.M., Tanez E., Zalacain M., "Similar short elements in the 5'
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"Similar short elements
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                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-31 FROM N.
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                                                                                                                                                                                                                                                                                                                                                                              Bacteriol. 169:2142-2149(1987).
                                                                                                                                                                                      GLUCOSE RESIDUES SUCCESSIVELY FROM WITH RELEASE OF BETA-D-GLUCOSE.
SIMILARITY: TO S. POMBE SPBC215.13.
                                                                                                                                                                                                                                  n Saccharomyces cerevisiae.";
5 Lett. 239:179-184(1988).
CATALYTIC ACTIVITY: HYDROLYSIS
                                                                                                                                                                          SIMILARITY: SOME, TO S.POMBE SPCC285.13C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LADTHWAAWAIKFATSOGLFKGYPDGTFKPDQNITRAEFATVVLHFLTKVKGQEIMSKLA
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                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
 Z38061;
M16164;
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   CAA86176.1;
AAA35014.1;
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                                                               license agreement (See http://www.isb-sib.ch/announce/
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EMBL; X13857; CAA32069.1;
PIR; B26877; B26877
PIR; A26877; A26877
PIR; A26877; A26877.
SCD; S0001458; MUC1.
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N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . . .) (POTENTIAL)
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AC P15941; P15942; P13931; P1762b; ~_

O1-JAN-1990 (Rel. 13, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

MUC1N 1 PRECURSOR (POLYMORPHIC EPITHELIAL MUCIN) (PEM) (PEM)

DE (EDISIALIN) (TUMOR-ASSOCIATED MUCIN) (CARCINOMA-ASSOCIATED MUCIN)

CTUMOR-ASSOCIATED EPITHELIAL MEMBRANE ANTIGEN)

REACTIVE URINARY MUCIN) (PUM) (BREAST CARCINOMA-ASSOCIATED ANTIGEN)

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MEDLINE-90368716; PubMed-2394722;

Lan M.S., Batra S.K., Q1 W.-N., Metzgar R.S.,

"Cloning and sequencing of a human pancreatic
J. Biol. Chem. 265:15294-15299(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Breast care
MEDLINE-90276413;
                                                                                                    "Structure and expression of the human gene: an expressed VNTR unit.";
                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-91097524; PubMed-2268309;
Lancaster C.A., Peat N., Duhig T.,
Taylor-Papadimitriou J., Gendler S
                                                                                                                                                                                                                                                                                                                   TISSUE-Breast carcinoma;

MEDLINE-90368715; PubMed-1697589;

Gendler S.J., Lancaster C.A., Taylor-Papadimitriou J., Du
Gendler S.J., Lancaster C.A., Taylor-Papadimitriou J., Du
Peat N., Burchell J., Pemberton L., Lalani E.-N., Wilson
"Molecular cloning and expression of human tumor-associat
polymorphic epithelial mucin.";
                                                 SEQUENCE FROM N.A.
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                       carcinoma;
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PubMed=2351132
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[9]
SEQUENCE OF 1-169 FROM N.A.
MEDLINE=90088473; PubMed=2597151;
Abe M., Siddiqui J., Kufe D.;
"Sequence analysis of the 5' region of the human [carcinoma-associated antigen gene.";
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                                                                                                                             Buluwela L., Liu Q., Submitted (OCT-1992)
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                                                                                                                                                    TISSUE-Breast
                                                                                                                                                                                                     MEDLINE=96181716; PubMed=8604237; Yu C.J., Yang P.C., Shew J.Y., Hou Lee L.N., Luh K.T., Wu C.W.; "Mucin mRNA expression in lung additissues.";
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                                                                                                                                                                                                                                                                                            Weiss M., Baruch A., Keydar I., Wreschner D.H., "Preoperative diagnosis of thyroid papillary os transcriptase polymerase chain reaction of the Int. J. Cancer 66:55-59(1996).
                                                                                                                                                                  SEQUENCE OF
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MEDILINE-91033045; PubMed-1688329;
TSarfaty I., Hareuveni M., Horev J., Z
Jeltsch J.M., Garnier J.M., Lathe R.,
"Isolation and characterization of an
coding for a breast-cancer-associated
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Keydar I.;
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. Biochem. 189:463-473(1990).
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A., Keydar I., Wreschner D.H.;
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J Z17325; CAA78973.1

J M31823; AAA35757.1

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30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation updat.
ADHESIVE PLAQUE MATRIX PROTEIN (POLYPHENOLI.
PROTEIN 1) (MEFP1) (FRAGMENT).
                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                  Repeat;
                                                                                                                                                                                                                                   InterPro: IPR002964; Adhesive_plaq.
InterPro: IPR002965; P_rich_extensn.
PRINTS; PR01216; ADHESIEI.
PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                              EMBL; X54422; CAA38294.1;
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      118
                         143
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MEDLINE-83135732;
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                                                                                                                                                                                                                                                                                                                                                         between
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Filpula D.R., Lee S.M., Link R.P., Str
"Structural and functional repetition
                                             60
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                                                                                                                                                                                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through a ween the Swiss Institute of Bioinformatics and the EMBI European Bioinformatics Institute. There are no restrictly non-profit institutions as long as its content is
                  PALTTPKEPTPTTPKE----PASTTPKEPTPTTIKSAPTTP-----KEPAPTTTKSAPTT
                                                                                                    TOHNKVSTSPKITTAKPINP------RP--SLPPNSDTSKETSLTVNKETTVET
PSSYKPKKTYPPTYKPKLTYPPTYKPKPSYPPTYKPKPSYPPSYKTKKTYPSSYKAKPSY
                                        PIKTTYNAKTNYPPVYKPKMTYPPTYKPKPSYPPTYKSKPTYKPKITYPPTYKAKPSY--
                                                     KETTTTNKQTSTDG--KEKTT---SAKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKG
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decapeptide in the adhesive
                                                                                                                          Score 556.5; DB 1;
Pred. No. 2.1e-16;
6; Mismatches 375;
                                                                                                                                                                                           TANDEM REPEATS OF Y-K-[PA]-K-[LP]-[ST]-Y-P-P-[ST].
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MEDLINE-99018118; PubMed-9799793; Glockner G., Scherer S., Schattevoy Tsui L.C., Rosenthal A.; "Large-Scale sequencing of
                                                                                                                                                                          ZAN_HUMAN STANDARD;

Q9Y493; 000218;

20-AUG-2001 (Rel. 40, Created)

20-AUG-2001 (Rel. 40, Last seq)

20-AUG-2001 (Rel. 40, Last ann)
                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
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Primates;
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on update)
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    'n
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                               Boright
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                                                                                                       Hominidae;
                            A
    chromosome
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-!- TISSUE SPECIFICITY: IN TESTIS; PRIMARILY IN HAPLOID SPERMATIDS.
-!- DOMAIN: THE MAM DOMAINS PROBABLY MEDIATE SPERM ADHESION TO THE ZONA PELLUCIDA.
-!- DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS,
THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF SPERMATOZOA OR PROMOTING ADHESION TO THE OVIDUCTAL ISTHMUS.
-!- DOMAIN: THE VWFD DOMAINS 2 AND 3 MAY MEDIATE COVALENT OLICOMERIZATION (BY SIMILARITY TO HUMAN INTESTINAL MUCIN MUC2).
-!- SIMILARITY: CONTAINS 3.5 MAM DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gao 2., Harumi T., Garbers D.L.;
"Chromosome localization of the mouse zona
zonadhesin gene (ZAN).";
Genomics 41:119-122(1997).
-!- FUNCTION: BINDS IN A SPECIES-SPECIFIC
OF THE EGG. MAY BE INVOLVED IN GAMETE
                                                                                                                                                                                                                                                                 Glycoprotein;
NON_TER
DOMAIN
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entities requires a license agreement (See
or send an email to license@isb-sib.ch).
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reveals 17
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                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR01217; PRICHEXTEN
SMART; SM00137; MAM; 2.
SMART; SM00214; VWC; 1.
SMART; SM00011; VWC_def; 3.
SMART; SM00216; VWD; 3.
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PS00740; MAM_1;
PS50060; MAM_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | IPR000998; MAM.
| IPR002965; P_rich
| IPR002919; TIL.
| IPR00328; TILA.
| IPR001007; VWFC.
| IPR001846; Vwd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genes.";
genes.";
8:1060-1073(1998).
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MAM 3.

MAM 4.

66 X HEPTAPEDTIDE REPEATS (AMAY 1.

(MUCIN-LIKE DOMAIN).

VWFD 1 (PARTIAL).

VWFD 2.

VWFD 3.

VWFD 4.

VWFD 4.

VWFD 5.

EGG-LIKE.

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                                                                                                                                                                                                                                                                                                                                                                                                  -PTTPTE-KPTIPTEKPTISTEKKPTIPTEK-PTISPEKLTIPTEKLTIPT---EKPTIPT
                                                                                                                                                         PTTPKEPAPT
                                                                                                                                                                              PPHPSPTA-TGLAALVMSPHAPSTPMTSV-
                                                                                                                                                                                                                                                                     KPTISPEKPTISTEK - - -
                                                                                                                                                                                                                                                                               199;
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    tabacum
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                                  (Rel. 13, Created)
(Rel. 13, Last sequence update)
(Rel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                STANDARD;
                                                                                                                                                           638
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                         st annotation update)
WALL HYDROXYPROLINE-
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N-LINKED
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Pred. No. 5.
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                                                                                 PRT;
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ED (GLCNAC...)
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                            -RICH GLYCOPROTEIN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 647
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                                                                                                                                                                                    966
                                                                                                                                                                                                                                                                        855
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Query Match 9.7
Best Local Similarity 27.7
Matches 170; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Specific expression of a novel cell wall hydroxyproline-rich glycoprotein gene in lateral root initiation."; Genes Dev. 3:1639-1646(1989).

"IF EUNCTION: HAS A SPECIALIZED STRUCTURAL FUNCTION, POSSIBLY THE MECHANICAL PENETRATION OF THE CORTEX AND EPIDERMIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana. NCBI_TaxID-4097;
                                                                                    400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-CV. XANTHI; MEDLINE-90128263; 1
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APTTPEEPTPTTPEEPAPTTPKAAAP----NTPKEPAPTTPKEPAPTTPKEPAPTTPKETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAIN ROOT.
SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX.
PTM: EXTENSINS CONTAIN A CHARACTERISTIC REE
                                    PPTPTPTFSPPPPAYSPPPTYSPPPPTYLPLSSPIYSPPPPYYSPPPPPSYSPPPPTYL
                                                                                                              RHLPPSPRRQPQPPTYSPPPPAYAQSPQPSPTYSPPPPTYSPPPPSPIYSPPPPAYSPSP
                                                                                                                                                  ---APTTPKEPSPTTTKEPAPTTPKEPAPTTPKKPAPTTPKEPAPT---TPKEPAPTTTK
                                                                                                                                                                                         PSPQV--QPPPT--YSPPPPTHVQPTPSPPSRGHQPQPPTHRHAPPTHRHAPPTHQPSPL
                                                                                                                                                                                                                             PAPTTPKEPAPTTPKEPAPTTTKEPSPTTPK---EPAPTTTKSAPTTTKEPAPTTTKS--
                                                                                                                                                                                                                                                                   P-----PSPSHGHAPPSGGHTPPRGQHPPSHRRPSPPSRHGHPPPPTYAQPPPTPIYS
                                                                                                                                                                                                                                                                                                     PAPTTPKKPAPT---TPKEPAPTTPKEPTPTTPKEPAPTTK--EPAPTTPKEPAPTAPKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            AETTTK-GPALTTP--KEPTPTT----PKEPASTTPKE---PTPTTIKSAPTTPKEPAP 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; X13885; CAA32090.1;
S06733; S06733.
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Cell wall;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         620
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151
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235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65406
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H-A-P-P.
A-P-P.
2 X 7 AA TANDEM REPEATS OF T-H-R-
1.
2.
CONTAINS THE SER-PRO(4) REPEATS.
3 X APPROXIMATE TANDEM REPEATS.
3 X APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
Pred.
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RESIDUE IS HYDROXYLATED AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTENSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       551;
No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TANDEM REPEATS OF T-H-R-H-A-P-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
.7e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Structural protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 620;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NFH_MOUSE STANDARD;
P19246; 061959;
01-NOV-1990 (Rel. 16, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-89121513; PubMed=3220257;
Cote F., Beaudet L.,
                                                                                                                                                                                                                                                                             Submitted
                                                                                                                                                                                                                                                                                                        STRAIN-SWISS WEBSTER;
                                                                                                                                                                                                                                                                                                                                             Shneidman P.S., Carden M.J., Lees J.F., Lazzarini R "The structure of the largest murine neurofilament revealed by cDNA and genomic sequences.";
Brain Res. 464:217-231(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Sequence and structure neurofilament subunit."; Gene 68:307-314(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Julien J.-P.,
Mushynski W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10090; [1]
                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=89089138; PubMed=3145094;
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                          EQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           589
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                           OF AXONAL CALIBER.

OF AXONAL CALIBER.

OF THE PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUI
OF THE LARGER NEUROFILAMENT POLYPEPFIZIDES (NF-M AND NP-H),
LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AI
COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION.
SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN IN POSITI-
TO 716 AND IS SHORTER DUE TO FRAMESHIFTS.
                                                                                                                                                 MILTED (MAR-1994) to the EMBL/GenBank/DDBJ databases.

FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, MAND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER. NE-H HAS AN IMPORTANT FUNCTION IN MATURE AXONS THAT IS NOT SUBSERVED BY THE TWO SMALLER NF PROTEINS.

PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P, NFH PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF: IT IS THOUGHT THAT PHOSPHORYLATION OF NFH RESULTS IN THE FORMATION OF INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTPKALENSPKEPGVPTTKTPAATKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPPRQIHSPPPPHWQPRTPTPTYGQPPSPPTFSAPPPRQIHSPPPPHRQPRPPTPTYGQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSP ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPPSPIYSPPPQVQPLPPTFSPPPPRRIHLPPPPPHRQP---RPPTPTYGQPPSPPTFSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                      TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Ver
Sciurognathi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
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thi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for
                                                                                                                                                                                                                                                                                                                                                                                           R.A.;
                                                                                                                                                                                                                                                                                                                                                                            protein (NF-H)
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; Murinae; Mus
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D.
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                                                                                                                                                     FORMATION OF
THE MAINTENANCE
                                                  POSITIONS
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EMBL; M35131; AAA39809.1; A
EMBL; M35131; AAA39809.1; A
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hes 216;
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                   P----APTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPA----PTTTKSAPTTTKEPAPTT
 PGEAKSPAEPKSPAEA--KSPA----EVKSPAEAKSPAEVKSPGEAKS-PAAVKSPAEAK
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JOINED.
ALT_FRAME.
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LINKER 12.

COIL 2A.

LINKER 2.

COIL 2B.

COIL 2B.

K -> QA (IN REF. 2 AND 3).
A -> AR (IN REF. 2 AND 3).
S -> T (IN REF. 2 AND 3).
L -> G (IN REF. 2 AND 3).
P -> PREAKSP (IN REF. 3).
MISSING (IN REF. 3).
G -> A (IN REF. 3).
G -> A (IN REF. 3).
T -> N (IN REF. 2 AND 3).
T -> N (IN REF. 2 AND 3).
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LINKER 1.
COIL 1B.
                                                                                                                                                                                                                                                              Score 533; DB 1;
Pred. No. 2.3e-15;
1; Mismatches 330
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50 x 6 AA TANDEM
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                                              EAKSPAEAKSPAEAKSPAEVKS
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01-NOV-1991
01-NOV-1991
20-AUG-2001
                                                                                                                          "Trypanosoma cruzi: localization of neur trypomastigotes.";
Trop. Med. Parasitol. 42:146-150(1991).
                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1991 (Rel. 20, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) SIALIDASE (EC 3.2.1.18) (NEURAMINIDASE) (NA)
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"The Trypanosoma cruzi neuraminidase contains bacterial neuraminidases, YWTD repeats of the bacterial neuraminidases of fibronectin.
                                                                                                                                                                                                                                                                                             MEDLINE=91277609; PubMed=1711561; Pereira M.E.A., Mejia J.S., Orteg
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-SILVIO X-10/4;
                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Euglenozoa;
NCBI_TaxID=5693;
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                    FUNCTION: DEVELOPMENTALLY REGULATED NEURAMINIDASE IMPLICATED PARASITE INVASION OF CELLS.

CATALYTIC ACTIVITY: HYDROLYSIS OF 2,3-, 2,6- AND 2,8-GLYCOSIDI LINKAGES JOINING TERMINAL NON-REDUCING N- OR O-ACYLNEURAMINYL RESIDUES TO GALACTOSE, N-ACETYLHEXOSAMINE, OR N- OR O-ACYLATER RESIDUES IN OLIGOSACCHARIDES, GLYCOPROTEINS, GLYCOLIPIDS OR COLOMINIC ACID.

SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (POSSIBLE).
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DEVELOPMENTAL STAGE: IN EPIMASTIGOTES AND
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174:179-191(1991)
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AND
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MAXIMAL ACTIVITY NO DETECTABLE IN
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PIR; JH0557; JH0557.
HSSP; P29768; 1DIL.
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BNR 1.
BNR 2.
BNR 3.
FIBRONECTIN TYPE-III.
44 X 12 AA TANDEM REPEATS, LTR DOMAIN.
N-LINKED (GLCNAC. . . ) (POTENTIAL).
                                                                                                            -PSTPADSSAHSTPSTPADSSAHSTPSTPVDSSAHSTPS
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Q1-OCT-1993
Q1-FEB-1994
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Calcium-bindi
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EMBL; L05080; AAA28420.1;
PIR; A47282; A47282.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       calcium and contains a leucine zipper.";
Proc. Natl. Acad. Sci. U.S.A. 90:1536-1540(1993).
-i- FUNCTION: MIGHT FUNCTION AS A CALCIUM-SEQUESTERING REGULAFE THE AMOUNT OF FREE CYTOPLASMIC CALCIUM. IT OF CA+2 PER MOL OF PROTEIN.
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CPN OR CAP
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"A Drosophila photoreceptor cell-specific protein, calcium and contains a leucine zipper.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93165729; PubMed=8094559;
Martin J.H., Benzer S., Rudnicka M., Miller C.A.;
"Calphotin: a Drosophila photoreceptor cell calcium-binding
"Proc. Natl. Acad. Sci. U.S.A. 90:1531-1535(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-CANTON-S;
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SUBCELLULAR LOCATION: CYTOPLASMIC;
TISSUE SPECIFICITY: SOMA AND AXONS
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Best Local :
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FP1_MYTCO ST/
Q25434;
30-MAY-2000 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 APTSKVLAKP-TPK---AETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PVAATPTPVVQIPVAAPVIATPPVAASAPTPAAVTPVISPVIASPPVVPANTTVPVAAPV 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPVSAPVAAPVTPSAVAAPVQVVSPAAVAP-----APAAPIAVTPVAPPPTLASVQPAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAVPAAVPVVAPVLAPAVAPAVAPVVAETPAPPPVAEIPVATIPECVAPLIPEVSVVATK 236
                                                                                                                                                                                                                                                                                                                                                                                                                        LAPTTTKEPTSTTSDKPAPTTPKGTAPTTP-----KEPAPTTPKEP--APTTPKGTAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                V----LPPVAAEPVPAVVAEETPETPAPASAPVTIAALDIPEVAPVIAAPSDAPAEAPSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPKEPAPTTPKEPAPTTPKETAPTTP-KGTAPTTLKE-----PAPTTPKKPAPKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAESIPAPVVATTPVPAT---LAVTDPDVTASAVPELPPVIAPSPVPSAVAETPVDLAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPEKL-APTTPEKPAPTTPEELAPTTPEEPTPTTPEEP---APTTPKAAAPNTPKEPAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ETPALAPVVAESQVAANTVVATPPTPAPEPET I APPVVAETPEVASVAVAETTPPVVPPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTTTKEP---APTTTKSAPTTPKEPSPTTTKEPA-PTTPKEPAPTTPKKPAPTTPKEPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PKEPA--PTAPKKPAPTTPKEPAPTTPKEPAPTTTKE-PSPTTPKEPAP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VTIPAPAPIAAASVTPVASVAPPVVAAPTP-----PAASPVSTPVAVAQIPVAVSAPVAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PKEPAPTTTKSAPTTP-KEPAPTTTKEPAPTTPKEPAPTTTKEPAPT----TTKSAPTTP
                                                                                                                                                                                                                                                                  SAEPTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKTTERDLRTTP--ETTTAAPKMT
                                                                                                                                                                                                                                                                                            EVAVAPITAPEPIP----EPEPSLATPTEPIPVEAPVVIQEAVDAVEVPVTETSTSIPET
                                                                                                                                                                                                                                                                                                                                                                    TLKEPA-----PTTPKKPAPKELAPTTT----KGPTSTTSDKPAPTT----PKETAPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLAAAEPVVVAPPATETPVVAPAAASPHVSVAPAVETAVVAPVSASTEPPVAAATLTTAP
                                                                                                                                                                                                                                                                                                                                                APPEAAADLIIEPVEPPAPIPDLLEQTTSVPAVEAAESTSS--PIPETSLPPPNEAVASP
                                                                                        LRDLQTTDVSLLAIAATLDAIGEKLKDQKARNQQVMDRLCEIEKILGPPKS
                                                                                                               PRKMTSTMPELNPTSRIAEAM----LQTTTRPNQTPNSKLVEVN----
                                                                                                                                          EVPITAGDNPDNTSVGISEVVPTIAEKPVEEVPTS--EIPEQSSSPS--DSVPVAKITPL
                                                                                                                                                                ITTTEIMNKPEETAKPKDRATNSKATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPKTTPT
                                                                                                                                                                                          DIAIPVIDPPVPQEIAVAEIPETDTKPAEVIVEQSTIPIEAPVPEVSKYAEPVISEAPAA
                                                                                                                                                                                                                  KETATTTEKTTESKITATTTQVTST-----TTQDTTPFKITTLKTTTLA-PKVTTTKKT
                                                                                                                                                                                                                                           TVE-FPEAVAEKVLDPAI--TEAPVTTQEPDVANINDGAPATEI-TTPAVEIVTAAAEVS
                                                                                                                                                                                                                                                                                                                      PKEPAPTTPKKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKSPD---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ΑĀ;
                                                                                                                                                                                                                                                                                                                                                                                                -TTASVPETTAPPAAVPTEPIDVSVLSEAAIETPVAPPVEVTTEVAVADV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -KEPAPTTTKKPAPTAPKEP---APTTPKET----APTTPKKLTPT
                          STANDARD;
  39,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84781 MW;
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  Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 530; DB 1;
Pred. No. 2.5e-15;
                             PRT;
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                             AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 152;
                                                                                                                    -PKS
                                                                                                                    895
                                                                                            864
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Best Local
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FP1.
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Mo
Mytiloidea; Mytilidae;
NCBI_TaxID=42192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mytilus coruscus (Sea
                                                                                                                                                                                                                                                                                                                DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96394686;
                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inoue K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                             186
                                                                       189
                                                                                               140
                     244
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                                                                                                                                                                        70
                    PAPTTPKEPAPTT
                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                   Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Takeuchi
                                                                                                                                                                                                                                                                                                             184
213
872
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21
124
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41
872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Adhesive protein cDNA sequence of the mussel Mytilus coruscus a its evolutionary implications.";

J. Mol. Evol. 43:348-356(1996).

-i- FUNCTION: PROVIDES ADHESIVENESS TO THE MUSSEL'S FOOT. MUSSEL PRODUCE ONE OF THE STRONGEST WATER INSOLUBLE GLUE. THE MUSSEL ADHESIVE IS A BUNDLE OF THREADS, CALLED A BYSSUS, FORMED BY FIBROUS COLLAGENOUS CORE COATED WITH ADHESIVE PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, I
20-AUG-2001 (Rel. 40, I
ADHESIVE PLAQUE MATRIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002964; Adhesive_plaq
InterPro; IPR002965; P_rich_extensn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D63777; BAA09850.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: SECRETED.
TISSUE SPECIFICITY: PRODUCED BY THE BYSSAL GLAND.
TISSUE SPECIFICITY: PRODUCED BY THE BYSSAL GLAND.
DOMAIN: ALMOST EXCLUSIVELY COMPOSED OF REPEATS OF A DECAPEPTIDE.
DOMAIN: ALMOST EXCLUSIVELY COMPOSED OF REPEATS OF A DECAPEPTIDE.
AND PTM: PROLLINES IN THE REPERT ARE HYDROXYLATED (SINGLE OR DI-) AND ALSO TYROSINE (THUS PRODUCING DOPA = 3,4-DIHYDROXYPHENYLALANINE).
                                                                                                                                                                                                                                                                                    VVDEAGSGLDNGDFKVTTPDTST--TQH-----NKVSTSPKITTAKPINPRPSLPPNS
                                                                                                                                                                                     YPTKRYQPTYGSKTNYPPIYKPIAKKLSSYKAIKTTYPAYKAKTSYPPSYK-----HKIT 139
                                                                                                                                                                                                                      DTSKETSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKDLAPTSKVL 129
                                                                                                                                                                                                                                                          VYGSAYSGASAYK-TLPGSHPYGSKHVPVYKPMNKIPT-PYI--SKKSYPAPYKPKGY
                                                                                                                   YPPTYK-----PKITYP--PTYKQKPSYPPSYKPKTTYPPTYK----PKITYPPTYK
                                                                                                                                                   AKPTPKAETTTKGPALTTPKEPT-PTTPKEPASTTPKEPTPTTTKSAPTTPKEPAPTTTK 188
                                                                                SAPT-TPKEPAPT--TTKEPAPTTPKEPAPTTTKEPAPTTTKSAPTTPKEPAPTT--PKK
                                                    RKPSYTPYKPKATYPPTYKPKITYP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PR01216; ADHESTVET.
PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydroxylation 1
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i Y., Takeyama S
                                                                                                                                                                                                                                                                                                                                                                                                               192
221
101677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ea mussel).
Mollusca;
                                                                                                                                                                                                                                                                                                                                            9.1%;
29.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
X PROTEIN PRECURSOR (FOOT
-PKEPTPTT--PKEPAPTTKEPAPTTPKEPAPT-APKKPAPTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mytilus
                                                                                                                                                                                                                                                                                                                              80;
                                                                                                                                                                                                                                                                                                                                                                                                                  M.
                                                                                                                                                                                                                                                                                                                            Score 518.5; 1
Pred. No. 7.3e
80; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADHESIVE PLAQUE MATRIX PROTEIN.
NONREPETIVE LINKER.
TANDEM REPEATS OF Y-K-[PS]-K-[IP]-[ST]-Y-P-[PST]-[ST].
                                                                                                                                                                                                                                                                                                                                                                                                                 NONAPEPTIDE 1.
NONAPEPTIDE 2.
NONAPEPTIDE 2.
NONAPEPTIDE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bivalvia; Pteriomorphia; Mytiloida,
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                                                       ·PTYKRKPSYT----
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                                                                                                                                                                                                                                                                                                                                                .3e-15;
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                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                407;
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                                                       -PYKPKTTYPPTYKPKI
                                                                                                                                                                                                                                                                                                                                                                                                                    CRC64;
                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coruscus and
                                                                                                                                                                                                                                                                                                                                                                    872;
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                                                                                                                                                                                                                                                                                                                                 181;
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                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                   69
                                                                                                                                                                                                                                                                 84
                                                           236
                                                                                                                             185
                                                                                         243
                          296
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"P-domains as shuffled cysteine-rich modules in ir C.1 (FIM-C.1) from Xenopus laevis. Polydispersity polymorphism.";
J. Biol. Chem. 267:24620-24624(1992).
"I-FUNCTION: COULD BE INVOLVED IN DEFENSE AGAINST
                                                                                                                                                                                  MUC1_XENLA STANDARD; PRT; 662 AA. 005049; 01-0CT-1994 (Rel. 30, Created) 01-0CT-1994 (Rel. 30, Last sequence update) 01-0CT-1994 (Rel. 30, Last annotation update) 1.TEGUMENTARY MUCIN C.1 (FIM-C.1) (FRAGMENT). Xenopus laevis (African clawed frog).
                                                                                           MEDLINE=93077556; PubMed=1447205;
Hauser F., Hoffmann W.;
                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Amphibia; Batrachia; Anura; M
                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                              NCBI_TaxID=8355
                                                                                                                                                       (enopodinae; Xenopus.
        INFECTIONS. PROTECTS THE EPITHELIA FROM SUBCELLULAR LOCATION: SECRETED. ALTERNATIVE PRODUCTS: A NUMBER OF DIFFE!
                                                                                                                                                                                                                                                                                                    YPPTYKPKISYPPTYKPKITYPPTYKPKISYPPAYKPKISYPSQ
                                                                                                                                                                                                                                                                                                                      MPRVRKPKTT--PTPRKMTSTMPELNPTSRIAEAMLQTTTRPNQ
                                                                                                                                                                                                                                                                                                                                                              VTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQ---KPTKAPKKP-TSTKKPK-T
                                                                                                                                                                                                                                                                                                                                                                                                       RTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTSTTTQDTTPFKITTLKTTTLAPK
                                                                                                                                                                                                                                                                                                                                                                                                                          Y---PPSYKPKKTYPPTYK----PKISYPPTYK----TKPSYPASYKRKTSYPPTYKPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPAPTTPKEPAPTTPKGTAPTTLKEPAPTTP----KKPAPKELAPTTTKGPTSTTSDKPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TT--PKGTAPTTLKEPAPTTPKKPAPKELAPTTTKEPTSTTSDKPAPT-TPKGTAPTTPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T-YKPKISYPPTYKPKASYVSSYKSKKTYPPTYKPKISYPPTYKPKPSYPPTYKPKITYP
                                                                                                                                                                                                                                                                                                                                                                                   ISYPSTYKAKP----SYPPTYKPKPSYASSYKPKIRYPPTYKPKPSYASSYK-----PK
                                                                                                                                                                                                                                                                                                                                                                                                                                              IHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAATKPEMTTTAKDKT----TERDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPTYKPKITYPPTYK-PKPSYPPSYRPKITYPPTYKPKKSYPQAYKSKGSYPPSYQPKKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTT--PKETAPTTPKEPAPTTPK--KPAPTTPET-----PPPTTSEVSTPTTTKEPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTYKPKITYPPTYK-----PKPSYPPSYKPKTTYPPTYKPKIRYPPTYKPKASYPPTYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APTAPKEPAPTTPKETAP-----TTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYKPKITYPPTYKPKPSYPPSYKPKKTYSPTYKPKITYPPTYKPKPSYPPSYKPKTTYPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     K-PKPSYPPTYKPKITYPPT-YKPKPSYPTPYKQKPSYPPIYKSKSSYPTSYKSKKTYPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPT----TTKEPAPTTTKSAPTTPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTYKPKPSYPPTYKPKITYPPTYKRKPSYPTYKQKPSYPPIYKSKSSYPTSYKSKKTYP
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Anura; Mesobatrachia; Pipoidea; Pipidae;
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-!- PTM: EXTENSIVELY O-GLYCOSYLATED.
-!- SIMILARITY: CONTAINS 6 P-TYPE ()
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E; PS00025;
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8 X APF
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LPQVADCKVAPSSR
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                    MPRVRKPKTTPTPR
                                                             KVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQKPTKAPKKPTSTKKPK---
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                                           TTTTTKATTTTTSGECKME - -
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EMBL; X74871; CAA52862.1; J
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EMBL; X74870; CAA52862.1; J
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P24928;
01-MAR-1992
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20-AUG-2001
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-i- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCE OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by the statement is not removed.
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Mammalia; Eutheria;
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                                                                                                                                                                                     InterPro; IPR000684; RNA_polII_repeat.
InterPro; IPR000722; RNA_pol_A.
InterPro; IPR002879; RNA_pol_A2.
Pfam; PF00623; RNA_pol_A; 1.
Pfam; PF01854; RNA_pol_A2; 1.
PROSITE; PS00115; RNA_POL_II_REPEAT; 43.
                                                                                                                                                                                                                                                                                                                                              PIR; S21054; S21054.
MIM; 180660; -
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SUBCELLULAR LOCATION: NUCLEAR.

THE TANDEM 7 RESIDUES REPEATS CAN BE HIGHLY PHOSPHORYLATED.

THE PHOSPHORYLATION ACTIVATES POL2.

MISCELLANEOUS: THERE DISTINCT ZINC-CONTAINING RNA POLYMERASES AR FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, CAND POLYMERASE II FOR SAND TRANA GENES.

III FOR 55 AND TRANA GENES.

SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBSTRATES.
CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE
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SUBUNIT: RNA POLYMERASE II CONSISTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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  DNA-directed RNA polymerase; Transcription; 2i
Nuclear protein; Phosphorylation; Zinc-finger.
71 87 CARBOXYL-TERMINAL 7-RESIDUE RE
590 1958 CARBOXYL-TERMINAL 7-RESIDUE RE
067 1067 W -> L (IN REF. 2).
449 1449 D -> Y (IN REF. 2).
970 AA; 217205 MW; 6876FC25692A657E CRC64;
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                                    Corden J.L., Cadena D.L., Ahearn J.M. Jr., Da "A unique structure at the carboxyl terminus of eukaryotic RNA polymerase II.";
                                                                                                                                                                                                                                                                                                    RPB1_MOUSE
P08775;
                         Proc. Natl.
                                                                                                       Ahearn J.M. Jr., Bartolomei M.S., West "Cloning and sequence analysis of the the largest subunit of RNA polymerase J. Biol. Chem. 262:10695-10705(1987).
                                                                                                                                                                                                                                 01-NOV 1988 (Rel. 09, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-001-001 (Rel. 40, Last annotation updat
DNA-DIRECTED RNA POLYMERASE II LARGEST SUBU
POLRZA OR RPO2-1 OR RPII215.
   REVISIONS,
                                                                      MEDLINE=86068017; PubMed=2999785;
                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=87280135; PubMed=3038894;
                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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MGD; MGI:98086; Rpo2-1.
InterPro; IPR000684; RNA_pol_A.
InterPro; IPR000722; RNA_pol_A.
InterPro; IPR002879; RNA_pol_A2.
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-I- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRA
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SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY
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MISCELLANEOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE
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                                                                                                                                                                                                                                                       -SPTSPSYSPTSPSY-SPTSPSYSPTSPSY-SPTSPSY-SPTSPSY-SPTSPSY-SPTSP
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Nuclear protein; Phosphorylation; Zinc
187 C2H2-TYPE (POTENTIAL).
71 SCRBOXYL-TERMINAL 7-RE
590 1958 CARBOXYL-TERMINAL 7-RE
498 1498 P -> R (IN REF. 1 AND
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Pred. No. 9.2e-14;
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MISSING (IN REF. 1 AND 2).
MW; 7D76F38FD9ZA657E CRC64;
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RESULT NEESULT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P16884; Q63368;
01-AUG-1990 (Rel. 15, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN)
(NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H) (FRAGMENT).
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Breen K.C., Robinson P.A., Wion D., Anderton B.H.
"Partial sequence of the rat heavy neurofilament
Identification of putative phosphorylation sites.
FEBS Lett. 241:213-218(1988).
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                            Lieberburg I., Spinner N., Snyder S., Anderson J., Goldgat
Smulowitz M., Carroll Z., Emanuel B.S., Breitner J., Rubir
"Cloning of a cDMA encoding the rat high molecular weight
neurofilament.peptide (NF-H): developmental and tissue exp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-89 AND 243-313 FROM N.A. MEDLINE=87080760; PubMed=2878828;
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Jolles P.;
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                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 318-831 FROM N.A. MEDLINE-89184647; PubMed-2928342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Robinson P.A., Wion D., Anderton B.H.; "Isolation of a cDNA for the rat heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem.
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FUNCTION: NSUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M, AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER. NET-H, HAS AN IMPORTANT FUNCTION IN MATURE AXONS THAT IS NOT SUBSERVED BY THE TWO SMALLER NF PROTEINS.

PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P, NFH IS PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF. IT IS THOUGHT THAT PHOSPHORYLATION OF NFH RESULTS IN THE FORMATION OF INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE
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ota; Metazoa; Chordata;
ia; Eutheria; Rodentia;
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PIM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTIO FIM: PHOSPHORYLATION SEEMS POLYPEPTIDES (NF-M AND NF-H), THE LEVELS OF PHOSPHORYLATION BEING ALTBRED DEVELOPMENTALLY AND COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION.

SIMILARTY: BELONGS TO THE INTERNEDIATE FILAMENT FAMILY.

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2: /cgn2_6/ptodata/2,

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Copyright (c) 1993 - 2000 Compugen Ltd
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ALIGNMENTS

Query Match Best Local Similarity

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522; DB 4; No. 7e-27;

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                                                    APPLICANT: Petersen,
TITLE OF INVENTION:
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PETERS, VERNY, JONES & Sherman Avenue, Suite
                                       PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS, THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM SPECIES INFECTIONS
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MOLECULE TYPE:
US-08-928-361B-5
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Matches
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TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1837 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA: US APPLICATION NUMBER: US
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STATE: C
COUNTRY:
                                                                                                                                                                                                                                                                                                                      487
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                                                                             727
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                  TTTTKRDEMTTTTPLPDIGDIEITPIPIEKMLDKYTRMIYDYNSGLLLDSNDEPIPGSQ
                                                                             AKYGAIHSGYQTSADFVTTTTAKPTTTTTGAPGQPTTTTTGSPSKPTTTTTKATTTTTI
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                                               PTTPKEPAPTTTKKPAP---
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21.3%; Pred. No. 1.5e-25;
tive 100; Mismatches 494; Indels 49
                                                                                                                                                                   -APTTPKEPAPTT---PKEPAPTTTKEPS-PTTPKEPAPTTTKS- 330
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RESULT 3
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; Patent No. 5202236
; Patent No. 5202236
; APPLICANT: MAUGH, KATHY J.; ANDERSON, DAVID M.; STRAUSBERG,
; SUSAN L.; MCCANDLISS, RUSS; WEI, TENA; FILPULA, DAVID
; TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
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NUMBER OF SEQUENCES: 39
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-MAY-1990
APPLICATION NUMBER: 82,456
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Best Local Similarity 29.9
Matches 239; Conservative
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APPLICATION NUMBER: 933,945
FILING DATE: 24-NOV-1986
APPLICATION NUMBER: 650,128
FILING DATE: 13-SEP-1984
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                            KETATTTEKTTESKITATTT
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                                                                                    PKEPGVPTTKTPAA-----TKPEMTTTAKDKTTERDLRTTPETTTAAP-----KMT
                                                                                                                  YKAKPSYPPTYKAKPSYPPTYKAKPSYPPTYKAKPSYPPTYKAKPTYKAKPTYPSTYKAK
                                                                                                                                                ---TPETPPPTTSEVSTPTTTKE----PTTIHKSPD-----ESTPELSAEPT-PKALENS
                                                                                                                                                                                PPTYKAKPTYK-AKPTYKAKPTYPSTYKAKPSYSPTYKAKPSYP----PTYKAKPSYPPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -APTTPKEPA--PTAPKKPA--PTTPKEPA--PTTPKEPA--PTTTKEPS--PTTPKEPA 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PKMTYPPTYKPKPSYPP-------TYKSKPTY-----KPKIT----
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                             759
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MOLECULE TYPE: PRINTER AND ANTI-SENSE: NO ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: Trich CRGANISME TYPE: PEUS-09-103-429A-3
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NAME: Michaels, Christopher A
REGISTRATION NUMBER: 34,390
REFERENCE, DOCKET NUMBER: BTI--
TELECOMMUNICATION INFORMATION:
TELEPHONE: (607) 256-2000
TELEPHONE: (607) 256-3628
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 786 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application Patent No. 6187558.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSE: Brown, Pinnisi & Michaels, P.C.
ADDRESSEE: Brown, 6187558th Tioga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: A No. 6187558el Invertebrate Intestinal Mucin TITLE OF INVENTION: cDNA and Related Products and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Granados, APPLICANT: Wang, Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 24-JUN-1998
CLASSIFICATION: 800
PTORNEY ACTIVE
                                                                                                                                                                                                                                                                                                                                                                  132 PTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTPTTIKSAPTTPKEPAPTTTKSAP 191
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                                                                                                                                                                     309
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OPERATING SYSTEM: PC-DOS/MS-DOS
362 CGAGTHFSFELQQCDHIELVGCTLPGGESEEVDVDEDA-CTGWYCPTEPIEWEPLPNGCP
                                                                                                                                   242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                    Match 8.7%;
Local Similarity 29.1%;
les 200; Conservative
                                                                                                                                                                                                                                                                    TTTQ--APTTTQ--ATTT---QAPTTTTQ-APTTTTQAPTTTTQ-APTTTQ--APTTTQ-
                                                                                                                                                                                                                                  PAPTTPKEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAPTT-PKEPA--
                                                                                                                                                                                                                                                                                       TTPKEPAPTTTKEPAPTTPKEPAPTTTKEPAPTTTKSAPTTPKEPAPTTPKKPAPTTPKE 251
                                                                                                                                                                                                                                                                                                                                     PGPPAE-TTQAPATT----QAPTTTQAPTTTT-----QAPTTTTQ--ATTTTQAP
                                                                  DGEISPAPPVTEGNEDEDIDIGDLLDNGCPANFEIDWLLPHGNRCDKYYQCVHGNLVERR
                                                                                                                                  ELLPNGCPADFDIHLLIPHDKYCNLFYQCSNGYTFEQRCPEGLYFNPYVQRCDSPANVEC
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                                                                                                                                                                                                                                                                                                                                                                                                         25;
                                                                                                                                                                                                                                                                                                                                                                                                         Score 498.5; DB 4;
Pred. No. 2.4e-25;
25; Mismatches 207;
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                                   -KSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKEP 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 786;
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US-08-700-651-5
Sequence 5, Application US/08700651B
Patent No. 6015882
GENERAL INFORMATION:
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Best Local Similarity
Matches 284; Conserv
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SEQ ID NO 5
LENGTH: 1721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF CRYPTOSPORTIGIUM PARVUM FILE OF INVENTION: INFECTIONS
FILE REFERENCE: 480.19-4 (HV)
CURRENT APPLICATION NUMBER: US/08/700,651B
CCURRENT FILING DATE: 1997-08-14
EARLIER FILING DATE: 1997-04-03
NUMBER: 05 LING DATE: 1995-04-03
NUMBER: 05 SEQ. ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: PETERSEN, CAI
APPLICANT: LEECH, JAMES
APPLICANT: GUT, JICH
APPLICANT: GUT, JICH
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                                                                     170
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                                                                                                                                                                                                                                                                            5 KKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRPS 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --PAPTAAPTAAPTTAAPESPTTVTVP-PTAAPTAAPTTAVPEIPITVT---SAPTAAPT 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAAPTT-AAPAPNTTVTVPPTAAPTAAPPTVAH-
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PTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPTPTTPKEPAPTTKEPAPTTPKEPAPTAPK 289
                                                                                                                                                                         APCNSENSFEQGQIFDMGSKVYIPYTKCVGVKHTTTTTTTTTTTTTTTT-
                                  TTIKSAPTTPKEPAPTTTKSAPTTPKEPAPTTTKEPAPTTPKEPAPTTTKEPAPTTTKSA 229
                                                                                                                                     ETQSIEKTSAKDLAPTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPASTTPKEPTP 169
                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                  Score 489; DB
Pred. No. 2.4e:
82; Mismatches
                                                                                                                                                                                                            ---TSLTVNKETTVETKETTTNKQTSTDGKEKTTSAK 109
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                                                                                                         DB 3;
?.4e-24;
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951 1258		918	1144			1024	798	964	739	916	696	857	674	799	628	741	571	681	531	628	471	581	411	527	369	467	358	407	350	351	290	301
PVDGLTTLRNGTLV 964	TKLPIPGSVAGDEILTEVLNITTDEVTGLP	MLSDETNICNGK	**************************************	1		NG				ELMYDIESGRLIGQVSKRPIPGSIAGDLNP	EPGVPTTKTPAATKPEMTTTAKDKTTER		PELSAEPTPKALENSPK 695	LTGYPLDPVSLIPFNPETGELFDPISDEINNGTIAGIVSGISASESLLSQKSALIDPA 856	APTTPKEPAPTTPKKPAPTTPETPPPTTSEVSTPTTTKEPTTIHKS 673				PKELAPTTTKEPTSTTSDKPAPTTPKG-TAPTTPKEPAPTT 570		KAAAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPA 530		0	FNEVYCDTCTAKYGA			APTTPKE 368	TSETESVIKPDEWCWLEKNGECEAKGATYVGVIGKDGRIENGMAFTMIPNDDTHVRFRFK 466	PKE	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT		

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 8.6%; Score 489; DB 3; Length 1721; Best Local Similarity 22.1%; Pred. No. 2.4e-24; Matches 284; Conservative 82; Mismatches 476; Indels 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NAMA:

APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(H)
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08928361B
Patent No. 6071518
GENERAL INFORMATION:
APPLICANT: Petersen, Carolyn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1721 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: PEP
TITLE OF INVENTION: THE
TITLE OF INVENTION: FOR
TITLE OF INVENTION: SPB
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0
          351
                    290 KPAPTTPKEPAPTTPKEPAPTTTKEPSPTTPKEDAPTTTKSAPTTTKEPAPTTTKSAPTT 3,49
                                                                                     301
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                                                                                                                                                                                                                                                                                                        159 APCNSENSFEQGQIFDMGSKVYIPYTKCVGVKHTTTTTTTTTTTTTTTTTTTTT------
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STREET: 385 Sheri
CITY: Palo Alto
STATE: CA
COUNTRY: USA
CIP: 94306-1840
                                                                                                                                                                                                                                                                                                                                            65 LPPNSDTSKE-----TSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                       5 KKNRTKKKPTPKPPVVDEAGSGLDNGDFKVTTPDTSTTQHNKVSTSPKITTAKPINPRPS
PTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTAPK 289
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385 Sherman Avenue, Suite 6
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PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,

THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS

FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
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                           RESULT 7
US-07-638-431-2
; Sequence 2, Application US/07638431
; Patent No. 5198535
; Patent INFORMATION:
; GENERAL INFORMATION:
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  Hoffman, Stephen
Charoenvit, Yupin
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                         Stephen L.
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NAME: Spevack, Avrom D.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 295-6759
TELEFAX: (301) 295-4033
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hedstrom, Richard
APPLICANT: Khusmith, Srisin
APPLICANT: Rogers IV, William O.
TITLE OF INVENTION: Protective malaria sporozoite surface protein
TITLE OF INVENTION: immunogen and gene
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
OPERATING SYSTEM: PC
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: A. David Spevack
STREET: NMRDC Building 1 T-12
STREET: Medical Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     273 TPCKVRDCPQIPIPPVIPNKIPEKPSNPEEPVNPNDPNDPNNPNNPNNPNNPNNPNNPNN 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168 TPTTIKSAPTTPKEPA-PTTTKSAPTTPKEPA-PTTTKEP----APTTPKEP-APTTTKE 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/07/638,431 FILING DATE: 19910110 CLASSIFICATION: 424
                                      571 PKEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
wes 153; Conserv
                                                                                                                                                                                                                                                                                                                                                                                            TKEPAPTTTKSAPTTPKEPSPTTTKEPAPTTPKEPA-PTTPKKP-APTTPKEPAPTTPKE 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTPEEPTPTTPEEPAPTTPKAAAPNTPKEP-APTTPKEPAPTTPKEPAPTTPKETAPTTP 510
                                                                                                                                                                                                                                                                                                                PAPTTTKKPAPTAPKEP-APTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAP 451
                                                                                                                                                                                                                                                                                                                                                        PNKPNP----NEPSNPNKPNPN----EPLNPNEPSNPNEPSNPNAPSNPNE---PSNPNE 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RRNPKRRNPNKPNKPNPNKPNPNEPSNPNKPNPN----EPSNPNKPNP----NEPSN 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAPTTTKSAPTTPKEP-APTTPKKP-APTTPKEP-APTTPKEP-TPTTPKEPAPTTKEPA 276
                                                                                                                SNPNE--PLNPNEP-----SNPNEPSNPNEPSNPEE--PSNPKE--PSNPNE
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AMINO ACID
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                                                                                        -PSNPEEPNPEE---PSNPKEP----SNPEEPINPEELNPKEPSNPEESN
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NPEESNPKEP----INPEDNENPLIIQDEPIEPRNDSNVIPI
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; Pred. No. 1.1e-24;
54; Mismatches 223;
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PCT-US92-00018-2
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (301) 295-4033
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US92/
FILING DATE: 19920103
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Spevack, Aviam D.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 195-6759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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APPLICANT:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 826 amino acids
TYPE: AMINO ACID
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PAPTTTKKPAPTAPKEP-APTTPKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAP
                                PNKPNP----NEPSNPNKPNPN-----EPLNPNEPSNPNEPSNPNAPSNPNE--PSNPNE
                                                             TKEPAPTTTKSAPTTPKEPSPTTTKEPAPTTPKEPA-PTTPKKP-APTTPKEPAPTTPKE 392
                                                                                                                                                                                           PAPTTTKSAPTTPKEP-APTTPKKP-APTTPKEP-APTTPKEP-TPTTPKEPAPTTKEPA 276
                                                                                            RRNPKRRNPNKPKPNKPNPNKPNPNEPSNPNKPNPN----EPSNPNKPNP----NEPSN 443
                                                                                                                             PTTPKEPAPTAPK--KPAPTTPKEPAPTTPKEPAPTTTKEPSPTTPKEPAPTTTKSAPTT 334
                                                                                                                                                              TPCKVRDCPQIPIPPVIPNKIPEKPSNPEEPVNPNDPNDPNNPNNPNNPNNPNNPNNPNN 332
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NMRDC Building 1 T-12 National Naval
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Khusmith, Srisin
Rogers IV, William O.
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Pred. No. 1.1e-24;
4; Mismatches 223;
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RESULT 9
5202236-13
; PATENT NO. 5202236
; APPLICANT: MAUGH, KATHY J.; ANDERSON, DAVID M.; STRAUSBERG,
; SUSAN L.; MCCANDLISS, RUSS; WEI, TENA; FILPULA, DAVID
; TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
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                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 82,456
FILLING DATE: 07-AUG-1987
APPLICATION NUMBER: 933,945
FILING DATE: 24-NOV-1986
APPLICATION NUMBER: 650,128
FILING DATE: 13-SEP-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/528,762
FILING DATE: 25-MAY-1990
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        253
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                              SAPTTTKEPA-----PTTTKSAPTTPKEPSPTTTKEPA--PTTPKEPA----PTTPKK 376
AKPTYKAKPTYKAKPTYPSTYKAKPTYP----PTYKAKPSYPPTYKAKPTYKAKPTYKAK
                                                                                      TPKEPAPTAPKKPA---PTTPKEPAPTTTKEPSPTTP-----KEPAPTTTK 329
                                                                  YP----PTYKAKPSYPPTYKAKPSYPPTYKAKPSYPPTYKAKPSYPSLIKAKPSYPPTYK 252
                                                                                                                                  PTYKPKPSYP--PSYKTKKTYPPTYKPKLTYPPTYKPKPSYPPSYKPNKTYPPTYKPKLT
                                                                                                                                                                 TTTKSAPTTPKEPAPTTPKKPAPT-TPKEPAPTT----PKEPTPTTPKEPAPTTKEPAPT 278
                                                                                                                                                                                                   SYPPTYKSKPTYKPKITYPPTYKAKPSYPPTYKPKKTYPPT-YKPKLTYPPTYKPKASYP 138
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                                                                                                                                                                                                                                                                                                                                        PKMTYPPTYKPKPSYPP------40
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29.7%; Pred. No. 5.3e-24;
7ative 71; Mismatches 284;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                               SEQ ID NO 5
                                                                                                                                Matches
                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: WIND, RICHELE D.

APPLICANT: VAN DEN BOSCH, TANJA J.

TITLE OF INVENTION: SILVER HALIDE EMULSIONS WITH RECOMBINANT COLLAGEN
TITLE OF INVENTION: SUITABLE FOR PHOTOGRAPHIC APPLICATION AND ALSO THE
TITLE OF INVENTION: PREPARATION THEREOF
                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 50
SOFTWARE: Date: 1998-12-23
                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/219,849
CURRENT FILING DATE: 1998-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE:
                                                                                                                                                                                                                                                                 LENGTH: 960
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                OTHER INFORMATION: OTHER INFORMATION:
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GPPGSRDPGPPGAPGPPGSRDPGPPGAPGPAGPPGSRDPGPPGAPGPAGPPGSRDPG 186
                             APTTPKEPAPTTKEPA-PTTPKEPAPTTTKEPAPTTTKSAPTTPKEPAPTTP---KKPA 245
                                                              PGPAGPPGSRDPG--PPGAPGPAGP--PGSRDPGPPGAPG-PAGPPGSRDPGPPGAPGPA 126
                                                                                                                                                  Similarity
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MOOBROEK, ANDREAS
WERTEN, MARC W.T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VAN HEERDE,
                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      2728-2
                                                                                                                                                                                                                                Description of Artificial Sequence: Illustrative amino acid sequence
                                                                                                                                                  25.6%;
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                                                                                                                                  Score 452; DB 4;
Pred. No. 3.3e-22;
0; Mismatches 309
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                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: PHARMACEUTICAL COMPOSITY TITLE OF INVENTION: TREATMENT OR PREVENTION
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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PRIOR APPLICATION DATA
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                                                                                  APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                               ZIP: 22313-1404
                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                 CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                   STREET:
              APPLICATION NUMBER: FR 9 FILING DATE: 23-OCT-1990
                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APTTPKKPAP-----KELAPTTTKGPTST--TSDKPAPTTPKETAPTTPKEPAPTTPKK 642
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                                                                                                                                                                                                                                                               Virginia
                                                                                                                                                                                                                                                                                                      P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                             HAREUVENI, Mara
                                                                                                                                                                                                                                                  United States
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAMBON,
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                                                                                                                                                                                                                                                                                                                   BURNS, DOANE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pierre
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                                                                                                        US/08/479,537A
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
TENGTH: 1867 amino acids
                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                              Matches
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REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 0177
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY:
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                                                                                                                                                            134 P-KAETTTKGP--ALTTPKEP------TPTTPKEPASTTPKEPTPTTIKSAP 176
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FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 0:
FILING DATE: 04-APR-1993
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LOCATION:
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OTHER INFORMATION:
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LOCATION: 128..1727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1867 amino ac
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
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         --DNKPAPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS 180
                                                                                          TTPKEPAPTTT-----KSAPTTPKEP------APTTTKEPAPTTPKEPAPTT 217
                                                                                                                            PGSGSSTTQGQDVTLAPATEPASGSAATWGQDVTSVPVTRPALGSTTPPAHDVT---SAP
                                                                                                                                                                                               TVLTV-----VTGSGHASSTPGGEKETSATQRSSVPSSTEKNAVSMTSSVLSSHS
                                                                                                                                                                                                                    TSLTVNKETTVETKETTTTNKQTSTDGKEKTTSAKETQSIEKTSAKD-LAPTSKVLAKPT 133
                                                                                                                                                                                                                                                                 7.4%; Score 424.5; DB 2;
ilarity 23.7%; Pred. No. 4.5e-20;
Conservative 69; Mismatches 511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
147
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21 amino
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which is
or ACG; a
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which is the codon for
or CCG; and Ala = GCT,
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no acid
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is the codon for Thr or Asn wherein
; and Asn = AAT or AAC."
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precursor s
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Pro or Ala wherein Pro =
GCC, GCA, or GCG."
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US-09-083-116-5
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                                                                                                                                                       Sequence 5, Application US/09083116 Patent No. 6203795 GENERAL INFORMATION:
                  TITLE OF INVENTION: PHARMACEUT TITLE OF INVENTION: TREATMENT NUMBER OF SEQUENCES: 5 CORRESPONDENCE ADDRESS:
                                                                                  APPLICANT: CHAMBON, Pierre
APPLICANT: KIENY, Marie-Paule
APPLICANT: LATHE, Richard
APPLICANT: HAREUVENI, Mara
                                                                                                                                                                                                                                                                         958 VTSAPDXRPXPGSTAPXAHGVTSA---
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                                                                                                                                                                                                                                                                                                       ETNICNGKPVDGLTT-LRNGTLVAFRGHYFWMLSPFSPPSPARRITEVWGIPSPID
                                                                                                                                                                                                                                                                                                                                                                        PNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLSD 942
                                                                                                                                                                                                                                                                                                                                                                                                                                             KPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPTSRIAEAMLQTTTRPNQT 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APDXRPXPG-----STAPXAHGVT-----SAPDXRPXPGSTAPXAHGVTSAPDXRPXP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -TKPEMTTTAKDK---TTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTS 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAP 762
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   BURNS,
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                                                PHARMACEUTICAL COMPOSITION FOR THE TREATMENT OR PREVENTION OF A MALIG
   DOANE,
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SWECKER & MATHIS, L.L.P.
                                                                                                                                                                                                                                                                                                                                           -----GVTSAPDXRPXPGSTA----PXAHG
                                                                                                                                                                                                                                                                         -PDXRPXPGSTAPXAHGVTSAPD 1003
                                                    MALIGNANT
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911

868

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571 530 471 468 419

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NAME/KEY: Peptide
; LOCATION: 1..21
; OTHER INFORMATION:
; OTHER INFORMATION:
US-09-083-116-5
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ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/083,116
FILING DATE:
CLASSIPITATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 0177:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEPAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1867 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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APPLICATION NUMBER: WO PCT/FR91/00835
FILING DATE: 23-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,320
FILING DATE: 04-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/403,576
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: TESKID, ROBID L.
SCHOOL STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATEMENT STATE
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APPLICATION NUMBER: (
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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OTHER INFORMATION:
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                                                                                                                                                                                                                               FEATURE:
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CITY: Alexandria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Peptide 
LOCATION: 147
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134
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                                                                                                                                                                                                                                                                     /note= "Amino acid 147 is X2 = Xaa
which is the codon for Pro or Ala wherein Pro = CCT, CCC,
or CCG; and Ala = GCT, GCC, GCA, or GCG."
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which is the codon for Pro or Ala wherein Pro = CCT,
or CCG; and Ala = GCT, GCC, GCA, or GCG."
                                                                                   /note= "Amino acids 1 to 21 are a 21 amino acid precursor sequence."
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OGNETY MECH. DOSETIONAL SAMILATITY 21.7%; SCOTE 414.5. DB 41. LONGTH 1867; DOSETIONAL SAMILATITY 21.7%; PROG. NO. 4.5 E. 20; MARCHES 255; CONSETTATIVE 69; MISMACCHES 511; Indels 211; Gaps 6, 16 17 TITTERE CONSETTATIVE 69; MISMACCHES 511; Indels 211; Gaps 6, 16 1 11. TITTERE CONSETTATIVE 69; MISMACCHES 511; Indels 211; Gaps 6, 17 17 TITRE PARTITION—ALTERSE OF 16 1 11. TITRE PARTITION—ALTERSE OF 17 TITRE PARTITION—ALTERSE OF 18 18 NEW-PARTITION—ALTERSE OF 18 NEW-PARTITION—ALTERSE OF 18 18 NEW-PARTITION—ALTERSE OF 18 18 NEW-PARTITION—ALTERSE OF 18 18 NEW-PARTITION—ALTERSE OF 18 18 NEW-PARTITION—ALTERSE OF 18 18 NEW-PARTITION—ALTERSE OF 18 18 NEW-PARTITION—ALTERSE OF 18 18 NEW-PARTITION—ALTERSE OF 18 18 NEW-PARTITION—ALTERSE OF 18 18 NEW-PARTITION—ALTERSE OF 18 18 NEW-PARTITION—ALTERSE OF 18 18 NEW-PARTITION—ALTERSE OF 18 18 NEW-PARTITION—ALTERSE OF 18 18 NEW-PARTITION—ALTERSE OF 18 18 NEW-PARTITION—ALTERSE OF 18 18 NEW-PAR																																				
MATCH SMAILARITY 23.7%; SCOTE 44.4.5; DB 4; Length 1867; cocal Similarity 23.7%; pred, No. 4.5e-20; cose 255; Conservative 69; Mismatches 511; Indels 24.1 daps 25.5; Conservative 69; Mismatches 511; Indels 24.1 daps 25.5; Conservative 69; Mismatches 511; Indels 24.1 daps 26.1	Qy	Db	Qy	Db	Qy	Db	Qу	Db	Qy	Db	Qy	Db	Qy	Db	ΩУ	Db	Qy	Db	Qy	Db	Qy	Вþ	Qy	Db	Qy	Db	Qy	Db	QΥ	Db	Qy	DЪ	Qy	Db	QУ	Que Bes
Si Conservative 23.7%; bred. No. 4.5 db 4. Length 1867; Si Conservative 69; mismatches 511; Indels 241; daps 55; Conservative 69; mismatches 511; Indels 241; daps 55; Conservative 69; mismatches 511; Indels 241; daps 55; Conservative 69; mismatches 511; Indels 241; daps 56; Conservative 69; mismatches 511; indels 241; daps 57; Conservative 69; mismatches 511; indels 241; daps 58; Conservative 69; mismatches 511; indels 241; daps 59; Conservative 69; mismatches 511; indels 241; daps 50; Conservative 69; mismatches 511; indels 241; daps 50; Conservative 69; mismatches 511; indels 241; daps 50; Conservative 69; mismatches 69; mism	4	\vdash	œ	6	2	N	6	o.	Ö	0	6	4	618	æ	7	w	Ñ	472	6	N	_	o	6	0	\vdash	241	6	181	218	2	177	66	134	6	S	
UI	ETNICNGKPVDGLTT-LRNGTLVAFRGHYFWMLSPFSPBRARRITEVWG1FSF1U 99	APXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHG 95	PNSKLVEVNPKSEDAGGAEGETPHMLLRPHVFMPEVTPDMDYLPRVPNQGIIINPMLSD 9	-GSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSA-PDXRPXPGST 9	KPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKNTSTMPELNPTSRIAEAMLQTTTRPNQT 8	APDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXP- 86	TTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETAKPKDRATNSKATTPKPQ 82	DXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS	-TKPEMTTTAKDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATTTQVTS 7	DXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAP 76	TTTKEPTTIHKSDDESTPELSAEPTPKALENSPKEPGVPTTKTPAA 7	RPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAP 7	KPAPTTPKETAPTTPKEPAPTTPKKPAPTTPETPPPTTSEVSTP 66	PXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAP-XAHGVTSAPDX	KEPAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTTTKGPTSTTSD 6	xAHGVTSAPDXRPXPGSTAP-XAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXR 5	KKPAPKELAPTITKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTP 5	PXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRP-XPGSTAPXAHGVTSAPDXRPXPGS 5	PKAAAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKGT-APTTLKEPAP 52	APDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGST 47	PKETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPAPT 46	APDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVT 41	APTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTTTKKPAPTAPKEPAPT 41	PDXRP-XPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVT 35	KEPSPTTPKEPAPTTTKSAPTTTKEPAPTTTKSAPTTPKEPSPTTTKE 36	PDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS 3	KEPAPTTKEPAPTTPKEPAPTAPKKPAPTTPKEPAPTT	: : DXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS 24	KEPAPTTTKSAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPTPTT 26	-DNKPAPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS 18	TPKEPAPTTTKSAPTTPKEPAPTTTKEPAPTTPKEPAPTT	GSGSSTTQGQDVTLAPATEPASGSAATWGQDVTSVPVTRPALGSTTPPAHDVTSAP	-KAETTIKGPALTTPKEPTPTIPKEPASTIPKEPTPTTIKSAP 17	TEKNAVSMTSSVLSSHS 6	SAKD-LAPTSKVLAKPT 13	h Similarity 23.7%; Pred. No. 4.5e-20; 55; Conservative 69; Mismatches 511; Indels 241; Ga

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US-08-479-537A-2
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                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 90/13101

FILING DATE: 23-OCT-1990

PRIOR APPLICATION NUMBER: WO PCT/FR91/00835

FILING DATE: 23-OCT-1991

PRIOR APPLICATION NUMBER: US 08/039,320

FILING DATE: 04-APR-1993
                                                                                                                                                                                                                                               TELEFAX: (703) 836-202
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2035 amino aci
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     FEATURE:
NAME/KEY:
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                                                                                                                                                                                                                                                                                                            NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REGERENCE/DOCKET NUMBER: 017753-025
TELECOMMUNICATION INFORMATION:
                                                                                                                  NAME/KEY: Peptide
LOCATION: 128.1899
OTHER INFORMATION: /n
OTHER INFORMATION: 12
OTHER INFORMATION: 20
                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 1
FILING DATE: 14-MAR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: PHARMACEUT
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                                         OTHER INFORMATION: OTHER INFORMATION:
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                            OTHER INFORMATION:
                                                                                                                                                                                                                   STRANDEDNESS:
                                                                   LOCATION:
                                                                                                         OTHER INFORMATION:
                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                  NAME/KEY:
                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Virginia
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LATHE, Richard
                                                                       Peptide
134
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14-MAR-1995
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836-2021
NO: 2:
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                        /note= "Amino acid 134 is X1 = Xaa
Xaa Xaa which is the codon for Pro or Ala wherein
CCC, CCA, or CCG; and Ala = GCT, GCC, GCA, or GCG.
                                                                                                  /note= "The amino acids spanning 128 to 1899 constitute a repeated region wherein the 20 amino acids, 17 of which are fixed. The number of repeats varies from 1 to 40."
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Best Local
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NAME/KEY:
703
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LOCATION:
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; OTHER INFORMATION: ; OTHER INFORMATION: US-08-479-537A-2
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OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
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                                                                                                                                                                                                                                                                                                                                                    APXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRP-XPGSTAPXAHGVTSAPDXRPXPGS
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DXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAP
                                     TTTKEPTT-----IHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAA-----
                                                                                 RPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGS--TAPXAHGVTSAP
                                                                                                                                                                       PXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAP-XAHGVTSAPDX
                                                                                                                                                                                                                      KEPAPTTPKG----TAPTTLKEPAPTTP-----
                                                                                                                                                                                                                                                                                                                                                                                                TPKA----AAPNTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGT-APTTLKEPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                        SAPDXRPXPGSTAPXAHGVTS----APDXRPXPGSTAPXAHGVTSAPDXRPX----PGST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TKE--PAPTTT-----KSAPTTPKEPAPTTPK----KPAPTTPKEPAPTTPKEPTPTT 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -- DNKPAPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTSAPDXRPXPGSTAPXAHGVTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTPKEPAPTTT-----KSAPTTPKEP------APTTTKEPAPTTPKEPAPTT 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TVLTV-----VTGSGHASSTPGGEKETSATQRSSVPSSTEKNAVSMTSSVLSSHS 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PKE--PAPTTKEP-----APTTPKEPAPTAPK----KPAPTTPKEPAPTTPKEPAPTT 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGSGSSTTQGQDVTLAPATEPASGSAATWGQDVTSVPVTRPALGSTTPPAHDVT---SAP 122
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                                                                                                                                  -ETAPTTPKEPAPTTP----
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23.78;
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which is
or CCG; a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Amino
21 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 424.5; DB 2;
Pred. No. 5e-20;
"" smatches 511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Amino acid
is the codon
3; and Ala = G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acids 1 to 21 are a precursor sequence."
                                                                                                                                                                                                                 ----KKPAPKELAPTTTKGPTSTTSD
                                                                                                                             -----KKPAPTTPETPPPTTSEVSTP 661
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1 for Pro or Ala wherein
GCT, GCC, GCA, or GCG."
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                                                    TELEFAX: (703) 836-2021 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/083,116
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                    APPLICATION NUMBER: US 01
FILING DATE: 04-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 14-MAR-1995
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                                                                                       REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: WO PCT/FR91/00835
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                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                   FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                               FILING DATE: 23-OCT-
PRIOR APPLICATION DATA:
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                                                                                                                                               NAME: Teskin, Robin L. REGISTRATION NUMBER: 35,030
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                 LENGTH:
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Best Local Similarity
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OTHER INFORMATION:
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FEATURE:
NAME/KEY: Peptide
LOCATION: 1..21
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LOCATION:
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   TPKA---
                                                             TPKETAP----TTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPT 468
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which is
or CCG; a
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which is the codon for Thr or
or ACG; and Asn = AAT or AAC."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Amino acid 134 is X1 = Xaa
Xaa Xaa which is the codon for Pro or Ala wherein
CCC, CCA, or CCG; and Ala = GCT, GCC, GCA, or GCG
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21 amino acid precursor sequence."
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Pred. No. 5e
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is the codon for Pro or Ala wherein; and Ala = GCT, GCC, GCA, or GCG."
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                                                                                                                                                                                                                                                                                                                                                                   Patent NO. 58340...
Patent NO. 58340...
GENERAL INFORMATION:
APPLICANT: Hardy, Daniel M.
APPLICANT: Garbers, David L.
APPLICANT: Species-Specific Egg-Binding Proteins
TITLE OF INVENTION: Sperm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08276967 Patent No. 5851817
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UTSD
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
TELEFAX: 713-789-2679
                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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STREET: F.
STREET: F.
TTTY: Houston
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                                                                                                                                              APPLICATION NUMBER: US/08/276,967 FILING DATE: Submitted Herewith
                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 77210-4433
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                                                                                                                               Submitted Herewith
                                                      UTSD:418\KIT
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Best Local Similarity
Matches 163; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 2476 amino acids
TYPE: amino acid
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TOPOLOGY: line
MOLECULE TYPE: I
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AHFERCACPVSCQ-SPTPNCEL
                                                                                                                                                 EKTTESKITATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEETA 806
                                                                                      KPKDRATNSKATTPKPQKPTKAPKKPTSTKKPKTMPRVRKPKTTPTPRKMTSTMPELNPT 866
                                                                                                                                                                                                                                                                                                                                                             GTAPTILKEPAPTTPKKPAPKELAPT-TTKGPTSTT---SDKPAPTTPKETAPTTPKEPA 636
                                                              AP-----TTPQP-SPTLVPTQPAAVVMPST----
                                                                                                                            ERTT-----TPTIRTTTPTERTT---IPTKKTT-----VPTEKTIIPT-----ERTI
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                                                                                                                                                                                                                             PKALENSPKEPGVPTTKTPAATKPENTTTAKDKTTERDLRTTPETTTAAPKMTKETATTT 746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSETSVSTEKPVAPTE----KPTVPSEIYTIPTEKPMVHMEKPIVHT--EKPTVPT-EKP 365
                               SRIAEAMLQTTTRPNQTPNSKL 888
                                                                                                                                                                                                                                                                                               PTTPKKPAPTTPETPPP----TTSEVSTPT----TTKEPTTIHKSPDESTPELSAEPT 686
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                                                              --SATTVTPRTTIASCP---PN
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Search completed: Job time: 231 sec April 26, 2002, 16:17:20

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